

## SEQUENCE LISTING

<110> Rock, Charles O  
Heath, Richard J

<120> Novel Enoyl Reductases and Methods of Use Thereof

<130> SJ-0022

<140> US 09/498,520

<141> 2000-02-04

<160> 62

<170> PatentIn version 3.1

<210> 1

<211> 975

<212> DNA

<213> Streptococcus pneumoniae

<400> 1

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<211> 324

<212> PRT

<213> Streptococcus pneumoniae

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20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys  
35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ser Leu Thr Asp Lys  
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Val Glu Asp Ile  
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala  
85 90 95

Gly Asn Pro Ser Lys Tyr Met Glu Arg Phe His Glu Ala Gly Ile Ile  
100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys  
115 120 125

Ile Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His  
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Ala Thr Ala  
145 150 155 160

Ile Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly Glu Gly  
165 170 175

Ala Ala Ala Gly Phe Met Leu Gly Ala Glu Ala Val Gln Val Gly Thr  
180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Pro Asn Tyr Lys Glu  
195 200 205

Lys Ile Leu Lys Ala Arg Asp Ile Asp Thr Thr Ile Ser Ala Gln His  
210 215 220

Phe Gly His Ala Val Arg Ala Ile Lys Asn Gln Leu Thr Arg Asp Phe  
225 230 235 240

Glu Leu Ala Glu Lys Asp Ala Phe Lys Gln Glu Asp Pro Asp Leu Glu  
 245 250 255

Ile Phe Glu Gln Met Gly Ala Gly Ala Leu Ala Lys Ala Val Val His  
 260 265 270

Gly Asp Val Asp Gly Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu  
 275 280 285

Val Ser Lys Glu Glu Thr Ala Glu Glu Ile Leu Lys Asp Leu Tyr Tyr  
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Val Arg Asn Asp

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 <213> Streptococcus mutans

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<212> PRT

<213> Streptococcus mutans

<400> 4

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20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys  
35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ala Val Thr Asn Lys  
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile  
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala  
85 90 95

Gly Asn Pro Gly Lys Tyr Ile Glu Arg Phe His Glu Ala Gly Ile Thr  
100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Arg Arg Met Glu Lys  
115 120 125

Leu Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His  
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Val Asp Ala  
145 150 155 160

Val Asn Ile Pro Val Ile Gly Ala Gly Gly Val Ala Asp Gly Arg Gly  
165 170 175

Ala Ala Ala Val Phe Met Leu Gly Ala Glu Ala Ile Gln Val Gly Thr  
180 185 190

Arg Phe Ala Val Ala Lys Glu Ser Asn Ala His Ala Asn Phe Lys Lys  
 195 200 205

Lys Ile Leu Lys Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Ser Ile  
 210 215 220

Val Gly His Pro Val Arg Ala Ile Lys His Lys Leu Ser Ser Ala Tyr  
 225 230 235 240

Ala Thr Ala Glu Lys Glu Phe Leu Arg Gly Glu Lys Ser Gln Glu Asp  
 245 250 255

Ile Glu Val Leu Gly Ala Gly Ala Leu Arg Asn Ala Val Val Asp Gly  
 260 265 270

Asp Val Asp Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Phe Val  
 275 280 285

Thr Lys Glu Glu Thr Cys Glu Glu Ile Leu Lys Asp Leu Tyr Tyr Gly  
 290 295 300

Ala Ala Lys Val Ile Lys Ala Glu Ala Ala Arg Trp Ala Asp Val Glu  
 305 310 315 320

Lys

<210> 5  
 <211> 972  
 <212> DNA  
 <213> Streptococcus pyogenes

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 attactgata gaccttttgg ggtaaatatc atgcttttat ctctttttgc tgatgatatc 240  
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<210> 6
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<213> Streptococcus pyogenes

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<400> 6

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Met Lys Thr Arg Ile Thr Glu Leu Leu Asn Ile Asp Tyr Pro Ile Phe
1           5           10           15

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Gln Gly Gly Met Ala Trp Val Ala Asp Gly Asp Leu Ala Gly Ala Val
          20           25           30

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Ser Asn Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
          35           40           45

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```

Glu Val Val Lys Ala Asn Ile Asp Arg Val Lys Ala Ile Thr Asp Arg
50           55           60

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Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
65           70           75           80

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Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
          85           90           95

```

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Gly Asn Pro Gly Lys Tyr Met Glu Arg Leu His Gln Ala Gly Ile Ile
          100          105          110

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Val Val Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
          115          120          125

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Leu Gly Val Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
          130          135          140

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Ile Gly Lys Leu Thr Thr Met Ser Leu Val Arg Gln Val Val Glu Ala
145           150          155          160

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Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly His Gly  
165 170 175

Ala Ala Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Ile Gly Thr  
180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Gln Asn Phe Lys Asp  
195 200 205

Lys Ile Leu Ala Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Gln Val  
210 215 220

Val Gly His Pro Val Arg Ser Ile Lys Asn Lys Leu Thr Ser Ala Tyr  
225 230 235 240

Ala Lys Ala Glu Lys Ala Phe Leu Ile Gly Gln Lys Thr Ala Thr Asp  
245 250 255

Ile Glu Glu Met Gly Ala Gly Ser Leu Arg His Ala Val Ile Glu Gly  
260 265 270

Asp Val Val Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Val  
275 280 285

Arg Lys Glu Glu Ser Cys Glu Thr Ile Leu Lys Asp Ile Tyr Tyr Gly  
290 295 300

Ala Ala Arg Val Ile Gln Asn Glu Ala Lys Arg Trp Gln Ser Val Ser  
305 310 315 320

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<211> 1068

<212> DNA

<213> Staphylococcus aureus COL

<400> 7

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cgccaattaa cgtcaaattc ttttggcgta aatgtctttg taccaagtca acaatcatat 240

accagtagtc aaattgaaaa tatgaatgca tgggttaaaac cttatcgacg cgcattacat 300

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atacatatgt ggagtggaca aagcccgcg ctagcaacaa cgcacccgc caacaccatc     1020
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<210> 8
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<212> PRT
<213> Staphylococcus aureus COL
<400> 8

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Ile Ile Gln Ala Gly Met Ala Gly Ser Thr Thr Pro Lys Leu Val Ala
          20          25          30

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```

Ser Val Ser Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
          35          40          45

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Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
          50          55          60

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Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
          65          70          75          80

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Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
          85          90          95

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Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
          100          105          110

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Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val  
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu  
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu  
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly  
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln  
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val  
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly  
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr  
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp  
 245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe  
 260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met  
 275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu  
 290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu  
 305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro  
 325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met  
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Gln Tyr Lys  
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<211> 999  
<212> DNA  
<213> Enterococcus faecalis

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aaagcgattg tacataagat gaatcagcgt tggggctaa 999

<210> 10  
<211> 332  
<212> PRT  
<213> Enterococcus faecalis

<400> 10

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20 25 30

Gly Met Ala Trp Val Ala Asp Ala Ser Leu Ala Ser Ala Val Ser Asn  
 35 40 45

Ala Gly Gly Leu Gly Ile Ile Ala Gly Gly Asn Ala Pro Lys Glu Val  
 50 55 60

Val Lys Lys Glu Ile Lys Lys Val Lys Glu Leu Thr Glu Gln Pro Phe  
 65 70 75 80

Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Glu Ile Val Asp  
 85 90 95

Leu Val Cys Glu Glu Gln Val Pro Val Val Thr Thr Gly Ala Gly Asn  
 100 105 110

Pro Ala Lys Tyr Met Ala Arg Phe Lys Glu His Asn Ile Lys Val Ile  
 115 120 125

Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys Ile Gly  
 130 135 140

Ala Asp Ala Val Ile Phe Glu Gly Met Glu Ala Gly Gly His Ile Gly  
 145 150 155 160

Lys Leu Thr Thr Met Ser Gly Leu Pro Gln Ile Val Asp Ala Val Ser  
 165 170 175

Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg Gly Met Ala  
 180 185 190

Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Leu Gly Thr Arg Phe  
 195 200 205

Leu Ile Ala Lys Glu Cys Asn Val His Pro Asp Tyr Lys Gln Lys Val  
 210 215 220

Leu Lys Ala Arg Asp Leu Asp Ala Val Ile Thr Cys Gln His Phe Gly  
 225 230 235 240

His Pro Val Arg Thr Leu Lys Asn Lys Leu Thr Ala Gln Tyr Asn Gln  
 245 250 255

Leu Glu Lys Gln Glu Leu Gln Lys Glu Val Pro Asp Leu Glu Met Phe  
 260 265 270

Glu Lys Ile Gly Gln Gly Ala Leu Arg Lys Ala Val Val Asp Gly Asp

275

280

285

Met Asp Tyr Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Lys  
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Lys Glu Glu Thr Ala Gln Glu Ile Ile Asp Ser Leu Met Ser Glu Cys  
 305 310 315 320

Lys Ala Ile Val His Lys Met Asn Gln Arg Trp Gly  
 325 330

&lt;210&gt; 11

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Clostridium acetobutylicum

&lt;400&gt; 11

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&lt;210&gt; 12

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Clostridium acetobutylicum

&lt;400&gt; 12

Met Leu Lys Thr Gln Phe Cys Asp Ile Ile Gly Ile Lys Tyr Pro Ile  
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Ile Gln Gly Gly Met Ala Trp Val Ala Asp Ser Ser Leu Ala Ala Gly  
 20 25 30

Val Ser Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Ala Asn Ala Pro  
 35 40 45

Val Glu Tyr Val Arg Asp Glu Ile Arg Lys Ala Lys Lys Leu Thr Asp  
 50 55 60

Lys Pro Phe Gly Val Asn Ile Met Leu Leu Ser Asp Asn Ala Glu Glu  
 65 70 75 80

Val Ala Lys Met Val Cys Glu Glu Gly Val Lys Val Val Thr Thr Gly  
 85 90 95

Ala Gly Asn Pro Gly Lys Tyr Ile Asp Met Trp Lys Glu His Asp Ile  
 100 105 110

Lys Val Ile Pro Val Val Ala Ser Val Ala Leu Ala Arg Arg Met Glu  
 115 120 125

Arg Cys Gly Val Asp Ala Val Val Ala Glu Gly Cys Glu Ser Gly Gly  
 130 135 140

His Val Gly Glu Leu Thr Thr Met Ala Leu Val Pro Gln Val Val Asp  
 145 150 155 160

Ala Ile Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg  
 165 170 175

Gly Val Ala Ala Ala Phe Ala Leu Gly Ala Ser Gly Val Gln Val Gly  
 180 185 190

Thr Arg Phe Leu Ile Ala Lys Glu Cys Thr Val His Gln Asn Tyr Lys  
 195 200 205

Asn Lys Val Leu Lys Ala Lys Asp Ile Asp Thr Glu Val Thr Gly Arg  
 210 215 220

Ser Thr Gly His Pro Val Arg Val Leu Arg Asn Lys Leu Ala Arg Lys  
 225 230 235 240

Tyr Lys Leu Met Glu Lys Glu Gly Ala Ser Pro Glu Glu Met Glu Glu

14

245

250

255

Leu Gly Arg Gly Ala Leu Pro Arg Ala Val Arg Glu Gly Asp Val Asp  
260 265 270

Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Asn Lys Glu  
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Glu Thr Cys Asp Glu Ile Val Glu Ser Met Phe Lys Glu Ala Val Glu  
290 295 300

Val Ile Asp Arg Ile Lys  
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<210> 13  
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<212> DNA  
<213> Clostridium difficile

<400> 13  
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acagataaac cttttggagt aaatgtaatg cttatgtgc catttgttga tgatataatt 240  
gatttgatta tagaagaaaa agttcaagtt attactactg gtgctggaaa tcctgcaaag 300  
tatatggata gattaaagga agctggaaca aagggttatt ctgtagtacc tacaatagct 360  
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ggaggacata taggagaact tactactatg gtcttagttc cacaagttgc tgatgctgta 480  
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gcattagggtg ccagtgcagt tcaagtagga actagattta ttgacagtga agagtgttct 600  
gtccattcaa actataaaaa cttagtacta aaagcaaaag atagagatgc aattgtaaca 660  
ggaagaagta ctggtcatcc agtaagaaca ttaaaaaata aactatcaa agaattttta 720  
aagatggaaac aaaatggagc tactcctgaa gaattggata aaaaaggtag aggagcttta 780  
agatttgcaa cagtagatgg agacatagaa aaagggtcat ttatggcagg tcaaagtgc 840  
gctatggtaa aagaaataac accttgtaag gaaattatag aggctatgg aaatcaagca 900  
agagagatta tgccagcaat agaactgtaa 930

<210> 14  
<211> 309  
<212> PRT

&lt;213&gt; Clostridium difficile

&lt;400&gt; 14

Met Asn Lys Ile Cys Lys Ile Leu Asn Ile Lys Tyr Pro Val Ile Gln  
 1 5 10 15

Gly Gly Met Ala Trp Val Ala Thr Ala Ser Leu Ala Ser Ala Val Ser  
 20 25 30

Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Gly Asn Ala Pro Lys Glu  
 35 40 45

Ala Ile Lys Lys Glu Ile Val Glu Cys Lys Lys Leu Thr Asp Lys Pro  
 50 55 60

Phe Gly Val Asn Val Met Leu Met Ser Pro Phe Val Asp Asp Ile Ile  
 65 70 75 80

Asp Leu Ile Ile Glu Glu Lys Val Gln Val Ile Thr Thr Gly Ala Gly  
 85 90 95

Asn Pro Ala Lys Tyr Met Asp Arg Leu Lys Glu Ala Gly Thr Lys Val  
 100 105 110

Ile Pro Val Val Pro Thr Ile Ala Leu Ala Gln Arg Met Glu Lys Leu  
 115 120 125

Gly Ala Thr Ala Val Ile Ala Glu Gly Thr Glu Gly Gly Gly His Ile  
 130 135 140

Gly Glu Leu Thr Thr Met Val Leu Val Pro Gln Val Ala Asp Ala Val  
 145 150 155 160

Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Val Asp Gly Arg Gly Ile  
 165 170 175

Ala Ala Ser Phe Ala Leu Gly Ala Ser Ala Val Gln Val Gly Thr Arg  
 180 185 190

Phe Ile Cys Ser Glu Glu Cys Ser Val His Ser Asn Tyr Lys Asn Leu  
 195 200 205

Val Leu Lys Ala Lys Asp Arg Asp Ala Ile Val Thr Gly Arg Ser Thr  
 210 215 220

Gly His Pro Val Arg Thr Leu Lys Asn Lys Leu Ser Lys Glu Phe Leu

225                      230                      235                      240  
 Lys Met Glu Gln Asn Gly Ala Thr Pro Glu Glu Leu Asp Lys Lys Gly  
                                  245                      250                      255  
 Thr Gly Ala Leu Arg Phe Ala Thr Val Asp Gly Asp Ile Glu Lys Gly  
                                  260                      265                      270  
 Ser Phe Met Ala Gly Gln Ser Ala Ala Met Val Lys Glu Ile Thr Pro  
                                  275                      280                      285  
 Cys Lys Glu Ile Ile Glu Ala Met Val Asn Gln Ala Arg Glu Ile Met  
                                  290                      295                      300  
 Pro Ala Ile Glu Leu  
 305

<210> 15  
 <211> 873  
 <212> DNA  
 <213> Porphyromonas gingivalis W83

<400> 15  
 atgaatagaa tttgcgaatt attgggtatc gaacatccga tcatatcggg aggcattggtg 60  
 tgggtgcagcg gttggaaact ggcttctgct gtgagcaact gcggtggttt gggacttatt 120  
 ggtgccggat ccatgcatcc ggacaatctg gagcatcaca tccgttcgtg taaagctgct 180  
 acagacaagc ctttcggtgt gaacgtgcct cttctctatc cggagatgga caaaatcatg 240  
 gagattatca tgagggaaca tgtgcccgtg gtggtaacgt cagccggtag tccaaagggtg 300  
 tggacagcca agttgaaagc tgccggtagc aagggtgatac atgtagttag cagtgccaca 360  
 ttcgctcgca aatcagaggc agccggtgta gacgccatcg tggccgaagg gttcgaagcc 420  
 ggcggacata atggacgaga ggagactacg accctctgtt tgatacctga agtagtggtat 480  
 gctgtgaaca ttcctgtggt tgctgccgga gggattgctt ccggccgtgc agttgccgct 540  
 gctttggctt tgggtgccga tgccgtacaa gtggggaccc gttttgctct gaggtaggaa 600  
 agttcggcgc atgaagactt taaggcacat tgccgcgggt cgggtggagg agatacgatg 660  
 ctttcgctca aggctgtatc gcctacgcga ctgctgaaga acaaattcta tcaggatgta 720  
 ttcgctgccg agcagcgcgg tgcttccgtg gaagagctgc gcgagctgct cggctcgtggt 780  
 cgtgccaaagc aaggtatttt cgaaggcgac ctgcacgagg gcgaattgga gataggccag 840  
 gcagtatcgc agataagtca tgcggagacg gtcg 873

<210> 16



<211> 313  
 <212> PRT  
 <213> Porphyromonas gingivalis W83

<400> 16

Met Asn Arg Ile Cys Glu Leu Leu Gly Ile Glu His Pro Ile Ile Ser  
 1 5 10 15

Gly Gly Met Val Trp Cys Ser Gly Trp Lys Leu Ala Ser Ala Val Ser  
 20 25 30

Asn Cys Gly Gly Leu Gly Leu Ile Gly Ala Gly Ser Met His Pro Asp  
 35 40 45

Asn Leu Glu His His Ile Arg Ser Cys Lys Ala Ala Thr Asp Lys Pro  
 50 55 60

Phe Gly Val Asn Val Pro Leu Leu Tyr Pro Glu Met Asp Lys Ile Met  
 65 70 75 80

Glu Ile Ile Met Arg Glu His Val Pro Val Val Val Thr Ser Ala Gly  
 85 90 95

Ser Pro Lys Val Trp Thr Ala Lys Leu Lys Ala Ala Gly Ser Lys Val  
 100 105 110

Ile His Val Val Ser Ser Ala Thr Phe Ala Arg Lys Ser Glu Ala Ala  
 115 120 125

Gly Val Asp Ala Ile Val Ala Glu Gly Phe Glu Ala Gly Gly His Asn  
 130 135 140

Gly Arg Glu Glu Thr Thr Thr Leu Cys Leu Ile Pro Glu Val Val Asp  
 145 150 155 160

Ala Val Asn Ile Pro Val Val Ala Ala Gly Gly Ile Ala Ser Gly Arg  
 165 170 175

Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Asp Ala Val Gln Val Gly  
 180 185 190

Thr Arg Phe Ala Leu Ser Glu Glu Ser Ser Ala His Glu Asp Phe Lys  
 195 200 205

Ala His Cys Arg Arg Ser Val Glu Gly Asp Thr Met Leu Ser Leu Lys  
 210 215 220

Ala Val Ser Pro Thr Arg Leu Leu Lys Asn Lys Phe Tyr Gln Asp Val  
225 230 235 240

Phe Ala Ala Glu Gln Arg Gly Ala Ser Val Glu Glu Leu Arg Glu Leu  
245 250 255

Leu Gly Arg Gly Arg Ala Lys Gln Gly Ile Phe Glu Gly Asp Leu His  
260 265 270

Glu Gly Glu Leu Glu Ile Gly Gln Ala Val Ser Gln Ile Ser His Ala  
275 280 285

Glu Thr Val Ala Glu Ile Met Val Asp Leu Val Asp Gly Tyr Lys Arg  
290 295 300

Ser Leu Ala Gly Met Pro Thr Glu Ile  
305 310

<210> 17  
<211> 966  
<212> DNA  
<213> *Caulobacter crescentus*

<400> 17  
atgggcctgc gcacgccgct gtgtgatctg ctggatatcg agcatccgat cctgctggcc 60  
ggcatgggcg gggctctcta cgtcccgtcg gccgccgccg tctccaacgc cggcggctat 120  
ggcgtcctgg gcatggccgg caccagcccg gacttcatcc gcgccagat gcgcgaggtc 180  
aaaagcctga ccgacaagcc gttcgggggtg gacctgctgg ccgccacgcc ggatgcgctg 240  
accgcgtccg tcgagggtcat catcgaggag ggcgcctcct catttgctgc gggcctgggc 300  
gtgcccctgc cgatcatcga acgactcaag gccgccggcc tgaagggtcat ggtcgtctgc 360  
ggagccgtga agcacgcggt caaggccgag caggcggggt gcgacgcggt gatctgcaa 420  
ggcggcgagg gcggtggtca cacgggtctc gtcggcaccc tgccgtggt ggcccaggcc 480  
gtggaggcgg tgaagatccc ggtggtcgcc gccggcggcc tgcacgacgg ccgcgggctg 540  
gcggcgcccc tggctctggg cgcgcagggc gtctggatgg gcacgcggtt catgcctcg 600  
cacgaggccc atgcgggcga tctctaccgc caggcgggtg tcgaggccgc cgacgaggac 660  
acggtgcgca cgcgctgcta ctcgggcaag ccgatgcggg tgaagaagaa cccctatgtc 720  
gacgactggg aagcgcgtcc cggcgacatc cagcccttcc cgcagcaggc catggtctcg 780  
atccgcaatg gcgccatggg cggcatcggc ggccagatcg agggcctgga cgcggccaag 840  
tcctgcttcg ccatgggcca gagcgccggc ggcgtgcgcg agatcttgcc ggccggcgag 900

atcgtcaagc ggctgatggc cgaggccgag acggcgctgg ccaaggcctc ggccttcagg 960  
acctga 966

<210> 18  
<211> 321  
<212> PRT  
<213> Caulobacter crescentus

<400> 18

Met Gly Leu Arg Thr Pro Leu Cys Asp Leu Leu Asp Ile Glu His Pro  
1 5 10 15

Ile Leu Leu Ala Gly Met Gly Gly Val Ser Tyr Ala Pro Leu Ala Ala  
20 25 30

Ala Val Ser Asn Ala Gly Gly Tyr Gly Val Leu Gly Met Ala Gly Thr  
35 40 45

Ser Pro Asp Phe Ile Arg Ala Gln Met Arg Glu Val Lys Ser Leu Thr  
50 55 60

Asp Lys Pro Phe Gly Val Asp Leu Leu Ala Ala Thr Pro Asp Ala Leu  
65 70 75 80

Thr Ala Ser Val Glu Val Ile Ile Glu Glu Gly Ala Ser Ser Phe Val  
85 90 95

Ala Gly Leu Gly Val Pro Leu Pro Ile Ile Glu Arg Leu Lys Ala Ala  
100 105 110

Gly Leu Lys Val Met Val Val Cys Gly Ala Val Lys His Ala Val Lys  
115 120 125

Ala Glu Gln Ala Gly Cys Asp Ala Val Ile Cys Gln Gly Gly Glu Gly  
130 135 140

Gly Gly His Thr Gly Leu Val Gly Thr Leu Pro Leu Val Ala Gln Ala  
145 150 155 160

Val Glu Ala Val Lys Ile Pro Val Val Ala Ala Gly Gly Leu His Asp  
165 170 175

Gly Arg Gly Leu Ala Ala Ala Leu Ala Leu Gly Ala Gln Gly Val Trp  
180 185 190

Met Gly Thr Arg Phe Ile Ala Ser His Glu Ala His Ala Gly Asp Leu

195

200

205

Tyr Arg Gln Ala Val Val Glu Ala Ala Asp Glu Asp Thr Val Arg Thr  
 210 215 220

Arg Cys Tyr Ser Gly Lys Pro Met Arg Val Lys Lys Asn Pro Tyr Val  
 225 230 235 240

Asp Asp Trp Glu Ala Arg Pro Gly Asp Ile Gln Pro Phe Pro Gln Gln  
 245 250 255

Ala Met Val Ser Ile Arg Asn Gly Ala Met Gly Gly Ile Gly Gly Gln  
 260 265 270

Ile Glu Gly Leu Asp Ala Ala Lys Ser Cys Phe Ala Met Gly Gln Ser  
 275 280 285

Ala Gly Gly Val Arg Glu Ile Leu Pro Ala Gly Glu Ile Val Lys Arg  
 290 295 300

Leu Met Ala Glu Ala Glu Thr Ala Leu Ala Lys Ala Ser Ala Phe Arg  
 305 310 315 320

Thr

<210> 19  
 <211> 987  
 <212> DNA  
 <213> Pseudomonas aeruginosa

<400> 19  
 atgggctgtg ttaggacccg ttccaccgag accttcggcg tcgaacaccc gatcatgcag 60  
 ggcggcatgc agtgggtcgg ccgtgccgag atggctgcgg cggaggccaa cgcgggtggc 120  
 ctggcgacgc tgcggcgtt gaccagccg agccggagg cactggctgc ggagattgcc 180  
 cgctgccgag agctgaccga tcggccgttc ggggtcaacc tgaccttgcg gccgacgcag 240  
 aagccgggtgc cctatgccga atatcgcgca gccatcatcg aggcgggaat ccgcgtcgtc 300  
 gaaaccgccc gcaacgaccc cggcgagcac atcgccgaat tccgtcgaca cggcgtcaag 360  
 gtgatccaca agtgaccgcg cgtgcgccat gcgtcaagg ccgagcgact gggcgtggac 420  
 gccgtctcca tcgacggctt cgagtgtgcc ggccaccgag gcgaggacga catccccggc 480  
 ctggtgttgc tgccggccgc ggccaaccgg ctacgcgtgc cgatcatcgc ctccggcggt 540  
 ttcgccgatg gacgtggcct ggctcgggcg ctggcgctgg gtgccgacgc gatcaacatg 600

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ggcacgcgct tcctggccac tcgcgaatgt ccgatacacc ctgcggtgaa ggcggcgatc 660
cgtgcgccgg acgagcggtc caccgacctg atcatgcggt ccctgcgcaa taccgcgccg 720
tgggcgcgca acgcgatcag ccaggaagta ctggcgatcg aggcacgcgg cggcgccggc 780
tacgccgata tcgccgcgct ggtcagcggc cagcgcggtc gccaggtgta ccagcagggc 840
gataccgacc tggggatctg gtcggccggc atgggtccagg gcctgatcga cgacgaaccg 900
gcctgcgccg agttgctcag ggacatcgtc gagcaggcgc gccaaactggt gcgtcaacgc 960
ctggagggca tgctcgccgg ggtctga 987

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```

<210> 20
<211> 328
<212> PRT
<213> Pseudomonas aeruginosa

```

```

<400> 20

```

```

Met Gly Val Phe Arg Thr Arg Phe Thr Glu Thr Phe Gly Val Glu His
1           5           10           15

```

```

Pro Ile Met Gln Gly Gly Met Gln Trp Val Gly Arg Ala Glu Met Ala
20           25           30

```

```

Ala Ala Val Ala Asn Ala Gly Gly Leu Ala Thr Leu Ser Ala Leu Thr
35           40           45

```

```

Gln Pro Ser Pro Glu Ala Leu Ala Ala Glu Ile Ala Arg Cys Arg Glu
50           55           60

```

```

Leu Thr Asp Arg Pro Phe Gly Val Asn Leu Thr Leu Leu Pro Thr Gln
65           70           75           80

```

```

Lys Pro Val Pro Tyr Ala Glu Tyr Arg Ala Ala Ile Ile Glu Ala Gly
85           90           95

```

```

Ile Arg Val Val Glu Thr Ala Gly Asn Asp Pro Gly Glu His Ile Ala
100          105          110

```

```

Glu Phe Arg Arg His Gly Val Lys Val Ile His Lys Cys Thr Ala Val
115          120          125

```

```

Arg His Ala Leu Lys Ala Glu Arg Leu Gly Val Asp Ala Val Ser Ile
130          135          140

```

```

Asp Gly Phe Glu Cys Ala Gly His Pro Gly Glu Asp Asp Ile Pro Gly
145          150          155          160

```

Leu Val Leu Leu Pro Ala Ala Ala Asn Arg Leu Arg Val Pro Ile Ile  
165 170 175

Ala Ser Gly Gly Phe Ala Asp Gly Arg Gly Leu Val Ala Ala Leu Ala  
180 185 190

Leu Gly Ala Asp Ala Ile Asn Met Gly Thr Arg Phe Leu Ala Thr Arg  
195 200 205

Glu Cys Pro Ile His Pro Ala Val Lys Ala Ala Ile Arg Ala Ala Asp  
210 215 220

Glu Arg Ser Thr Asp Leu Ile Met Arg Ser Leu Arg Asn Thr Ala Arg  
225 230 235 240

Val Ala Arg Asn Ala Ile Ser Gln Glu Val Leu Ala Ile Glu Ala Arg  
245 250 255

Gly Gly Ala Gly Tyr Ala Asp Ile Ala Ala Leu Val Ser Gly Gln Arg  
260 265 270

Gly Arg Gln Val Tyr Gln Gln Gly Asp Thr Asp Leu Gly Ile Trp Ser  
275 280 285

Ala Gly Met Val Gln Gly Leu Ile Asp Asp Glu Pro Ala Cys Ala Glu  
290 295 300

Leu Leu Arg Asp Ile Val Glu Gln Ala Arg Gln Leu Val Arg Gln Arg  
305 310 315 320

Leu Glu Gly Met Leu Ala Gly Val  
325

<210> 21

<211> 1044

<212> DNA

<213> Bacillus subtilis

<400> 21

atgaatgaat ttatgaaaaa gttttcttta acaaaaccga ttattcaagc tccaatggct 60  
ggcgggtatta caaagccccg acttgcacat gcagtttcga atcaaggtgc tcttggcagc 120  
ttagcatcgg ggtatcttac gccagacctc ctagaacaac aaataaaaaga aatatttgag 180  
ctgacagacg ctctttttca aattaatgtg tttgttccgc taggtctaga gatgccacca 240  
aaagatcaga ttaaaaagtg gaaagaaaac ataccgttag ctaatcaagt aaatcaattc 300

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acatctgtac aagaagagtg ggatgacttc tatcaaaaaa ttgatctaata tttaaaatac 360
aagggttaagg cttgctcatt cacttttgat ctgccgcctg aagacgcagt aaaggagcta 420
aaaaccgctg gatgctgttt aataggaacc gcttcaacag tagaagaagc attgttaatg 480
gaagaacggg gaatggatat agtagtcctt caaggaagtg aagccggtgg acatcgcgga 540
gcattcttac cttccaaagg tgaatctgcc gtaggttttaa tggctctgat tccacaagca 600
gcagatgcac tgagcgtacc tgtcatagct gctgggggaa tgatagacca cagaggagta 660
aaagcagctt taaccctcgg agcccaaggc gttcaaatac gttctgcctt tttaattgt 720
cacgagagta acgcacatcc agtgcataaa cagaaaatac tagaagcaaa cgaagcagat 780
acaaagctta cgacattatt ttcaggtaaa gaggccagag gaatcgtaaa taaatggatg 840
gaagaaaatg aacagtttga gacacaaacc cttccgtacc cttatcaaaa tacactaacg 900
aaggcaatga gacagaaggc ttcacttcaa aataaccatg atcagatgtc tttatgggca 960
ggtcaaggga tacggtcatt gactgaggaa atttcgggta agcagctttt aaatcagctt 1020
tgccaagagg atataaaaat atag 1044

```

```

<210> 22
<211> 347
<212> PRT
<213> Bacillus subtilis

```

```

<400> 22

```

```

Met Asn Glu Phe Met Lys Lys Phe Ser Leu Thr Lys Pro Ile Ile Gln
1           5           10           15

```

```

Ala Pro Met Ala Gly Gly Ile Thr Lys Pro Arg Leu Ala Ser Ala Val
20           25           30

```

```

Ser Asn Gln Gly Ala Leu Gly Ser Leu Ala Ser Gly Tyr Leu Thr Pro
35           40           45

```

```

Asp Leu Leu Glu Gln Gln Ile Lys Glu Ile Phe Glu Leu Thr Asp Ala
50           55           60

```

```

Pro Phe Gln Ile Asn Val Phe Val Pro Leu Gly Leu Glu Met Pro Pro
65           70           75           80

```

```

Lys Asp Gln Ile Lys Lys Trp Lys Glu Asn Ile Pro Leu Ala Asn Gln
85           90           95

```

```

Val Asn Gln Phe Thr Ser Val Gln Glu Trp Asp Asp Phe Tyr Gln
100           105           110

```

Lys Ile Asp Leu Ile Leu Lys Tyr Lys Val Lys Ala Cys Ser Phe Thr  
 115 120 125

Phe Asp Leu Pro Pro Glu Asp Ala Val Lys Glu Leu Lys Thr Ala Gly  
 130 135 140

Cys Cys Leu Ile Gly Thr Ala Ser Thr Val Glu Glu Ala Leu Leu Met  
 145 150 155 160

Glu Glu Arg Gly Met Asp Ile Val Val Leu Gln Gly Ser Glu Ala Gly  
 165 170 175

Gly His Arg Gly Ala Phe Leu Pro Ser Lys Gly Glu Ser Ala Val Gly  
 180 185 190

Leu Met Ala Leu Ile Pro Gln Ala Ala Asp Ala Leu Ser Val Pro Val  
 195 200 205

Ile Ala Ala Gly Gly Met Ile Asp His Arg Gly Val Lys Ala Ala Leu  
 210 215 220

Thr Leu Gly Ala Gln Gly Val Gln Ile Gly Ser Ala Phe Leu Ile Cys  
 225 230 235 240

His Glu Ser Asn Ala His Pro Val His Lys Gln Lys Ile Leu Glu Ala  
 245 250 255

Asn Glu Ala Asp Thr Lys Leu Thr Thr Leu Phe Ser Gly Lys Glu Ala  
 260 265 270

Arg Gly Ile Val Asn Lys Trp Met Glu Glu Asn Glu Gln Phe Glu Thr  
 275 280 285

Gln Thr Leu Pro Tyr Pro Tyr Gln Asn Thr Leu Thr Lys Ala Met Arg  
 290 295 300

Gln Lys Ala Ser Leu Gln Asn Asn His Asp Gln Met Ser Leu Trp Ala  
 305 310 315 320

Gly Gln Gly Ile Arg Ser Leu Thr Glu Glu Ile Ser Val Lys Gln Leu  
 325 330 335

Leu Asn Gln Leu Cys Gln Glu Asp Ile Lys Ile  
 340 345



<210> 23  
 <211> 1128  
 <212> DNA  
 <213> Mycobacterium tuberculosis rv1533

<400> 23  
 atgcggaacca gagtcgcca gctgctcggg gctgagtttc caatatgcgc gttcagccac 60  
 tgccgggatg tgggtggcggc ggtgtccaat gcggtgcgggt tcgggatcct cggtgccgtc 120  
 gcacatagcc ccaaaccggct ggagagcgag ctgacctgga tcgaggagca cacgggtggc 180  
 aagccgtacg gagtcgacgt gctgctgccg cccaaatata tcggcgccga gcaaggcggc 240  
 atcgatgccc agcaggcccc ggagctcata cccgaagggc atcgcacctt cgtcgacgac 300  
 ttgctgggtc gctatggcat ccccgcggtc accgaccggc agcggttcgtc ctccggccgt 360  
 gggctgcaca tctcgcccaa gggttatcag ccgttgctgg atgtggcctt cgcccatgac 420  
 atccggttga tcgccagcgc gctcggggcg ccgccaccgg atctcgtgga gcgcgcccac 480  
 aaccatgacg tgctgggttc cgccctagcc ggacacggcg agcacgcgcg gcgacacgcg 540  
 gctgcgggtg ttgacctgat cgtcgcgagc ggacaccgag ccggaggcca caccggcgag 600  
 gtggcgacca tgggttctgg tcccgaagtc gtcgatgcgg tgcgccaac gccggtgctg 660  
 gccgcggggc ggatcgcccc tggccgccag atcgctgcgg cgttgggcctt gggggcgga 720  
 ggcgtctggt gcgggtcggc ctggttgacc accgaagaag ccgaaacgcc cccggtggtc 780  
 aaggacaagt ttctggccgc aacatcctcg gacacgggtg ggtcccggtc gctaaccggc 840  
 aagccggcgc gcatgctgcg cacggcctgg accgacgaat gggatcgccc tgacagcccc 900  
 gaccgccttg gcatgccgct gcagagcgcg ctggtcagcg accgcagtt gcgcatcaac 960  
 caggccgcgc gccagcccgg ggccaaggct cgtgagctgg cgacctactt cgtcggacag 1020  
 gtcgtcggct cactcgaccg ggtgcggctc gccgcctcgg tgggtgcttga catggtcgag 1080  
 gagttcatcg acaccgtcgg gcaactgcag ggggttggtc aaaggtga 1128

<210> 24  
 <211> 375  
 <212> PRT  
 <213> Mycobacterium tuberculosis rv1533

<400> 24

Met Arg Thr Arg Val Ala Glu Leu Leu Gly Ala Glu Phe Pro Ile Cys  
 1 5 10 15

Ala Phe Ser His Cys Arg Asp Val Val Ala Ala Val Ser Asn Ala Gly  
 20 25 30

Gly Phe Gly Ile Leu Gly Ala Val Ala His Ser Pro Lys Arg Leu Glu

35

40

45

Ser Glu Leu Thr Trp Ile Glu Glu His Thr Gly Gly Lys Pro Tyr Gly  
50 55 60

Val Asp Val Leu Leu Pro Pro Lys Tyr Ile Gly Ala Glu Gln Gly Gly  
65 70 75 80

Ile Asp Ala Gln Gln Ala Arg Glu Leu Ile Pro Glu Gly His Arg Thr  
85 90 95

Phe Val Asp Asp Leu Leu Val Arg Tyr Gly Ile Pro Ala Val Thr Asp  
100 105 110

Arg Gln Arg Ser Ser Ser Ala Gly Gly Leu His Ile Ser Pro Lys Gly  
115 120 125

Tyr Gln Pro Leu Leu Asp Val Ala Phe Ala His Asp Ile Arg Leu Ile  
130 135 140

Ala Ser Ala Leu Gly Pro Pro Pro Pro Asp Leu Val Glu Arg Ala His  
145 150 155 160

Asn His Asp Val Leu Val Ala Ala Leu Ala Gly Thr Ala Gln His Ala  
165 170 175

Arg Arg His Ala Ala Ala Gly Val Asp Leu Ile Val Ala Gln Gly Thr  
180 185 190

Glu Ala Gly Gly His Thr Gly Glu Val Ala Thr Met Val Leu Val Pro  
195 200 205

Glu Val Val Asp Ala Val Ser Pro Thr Pro Val Leu Ala Ala Gly Gly  
210 215 220

Ile Ala Arg Gly Arg Gln Ile Ala Ala Ala Leu Ala Leu Gly Ala Glu  
225 230 235 240

Gly Val Trp Cys Gly Ser Val Trp Leu Thr Thr Glu Glu Ala Glu Thr  
245 250 255

Pro Pro Val Val Lys Asp Lys Phe Leu Ala Ala Thr Ser Ser Asp Thr  
260 265 270

Val Arg Ser Arg Ser Leu Thr Gly Lys Pro Ala Arg Met Leu Arg Thr  
275 280 285

Ala Trp Thr Asp Glu Trp Asp Arg Pro Asp Ser Pro Asp Pro Leu Gly  
 290 295 300

Met Pro Leu Gln Ser Ala Leu Val Ser Asp Pro Gln Leu Arg Ile Asn  
 305 310 315 320

Gln Ala Ala Gly Gln Pro Gly Ala Lys Ala Arg Glu Leu Ala Thr Tyr  
 325 330 335

Phe Val Gly Gln Val Val Gly Ser Leu Asp Arg Val Arg Ser Ala Arg  
 340 345 350

Ser Val Val Leu Asp Met Val Glu Glu Phe Ile Asp Thr Val Gly Gln  
 355 360 365

Leu Gln Gly Leu Val Gln Arg  
 370 375

<210> 25  
 <211> 1035  
 <212> DNA  
 <213> Mycobacterium tuberculosis rv2781c

<400> 25  
 atggtgttgg gcttctggga catcgcggtg ccgatcgctg gcgccccgat ggccggcggc 60  
 ccgagcacc cggcggttggc cgcggcggtg tccaacgctg gcgggcttgg ttctgctgcc 120  
 ggcggctatc tgagcgcgga ccggctcgcc gacgatatcg ccgctgcgcg gcgcgccact 180  
 accggtccta tcggagccaa tctgtttgtg ccccaacca gcgtcgccga ctgggcgcag 240  
 ctggagtatt acgcggacga gtcgaagag gtgcgcgagt actaccacac cgagggtgggc 300  
 cagcccgctc atggtgacga cgacgactgg gtgcgcaaac tcgaggtggg agccgatggt 360  
 cgtccggagg tgggtgctgt caccttcggc gcgcgcgcgc cggatgtcgt gcagcggttg 420  
 agcgcgctgg gactgttggg ctcgatcacc gtgacgtcgg tctacgaggc cgggtgtggcc 480  
 attgccgcgg gcgcggacag cctggtgggc cagggcccg gcgcggcg gcaccgcgga 540  
 acgttcgcgc cggacatgga acccggtacg gagtcgctgc accaactcct cgatcggatt 600  
 ggcagcgccc atgatgtgcc gctggttgca gccgggtggc tgggcacggc tgaggacgtg 660  
 gccgccgtgc tgcgcgcgg agcgatcgcc gcgcagggtg gtaccgcatt gctgctggcc 720  
 gacgaagccg gtaccaatgc cgcacaccgt gccgcgctga agaatccaga gttcgatgcc 780  
 accctgggtc ctcgggcgtt ctcgggtagg tatgcgcgcg gtctggccaa caacttact 840  
 cgctgctcg accacgtggc gccgctgggt tatccggagg tccaccagat gacgaagccg 900

atacgggagg cgagggtgca ggaggacgac ccgcacggaa caaacctttg ggagggatcg 960  
 gcgcaccgga agaccgggcc ggagcccgcg gccgacatca tcgcttcct tactcccgac 1020  
 gtgtgctcgg cgtaa 1035

<210> 26  
 <211> 344  
 <212> PRT  
 <213> Mycobacterium tuberculosis rv2781c

<400> 26

Met Val Leu Gly Phe Trp Asp Ile Ala Val Pro Ile Val Gly Ala Pro  
 1 5 10 15

Met Ala Gly Gly Pro Ser Thr Pro Ala Leu Ala Ala Val Ser Asn  
 20 25 30

Ala Gly Gly Leu Gly Phe Val Ala Gly Gly Tyr Leu Ser Ala Asp Arg  
 35 40 45

Leu Ala Asp Asp Ile Ala Ala Ala Arg Ala Ala Thr Thr Gly Pro Ile  
 50 55 60

Gly Ala Asn Leu Phe Val Pro Gln Pro Ser Val Ala Asp Trp Ala Gln  
 65 70 75 80

Leu Glu Tyr Tyr Ala Asp Glu Leu Glu Glu Val Ala Glu Tyr Tyr His  
 85 90 95

Thr Glu Val Gly Gln Pro Val Tyr Gly Asp Asp Asp Asp Trp Val Arg  
 100 105 110

Lys Leu Glu Val Val Ala Asp Val Arg Pro Glu Val Val Ser Phe Thr  
 115 120 125

Phe Gly Ala Pro Pro Pro Asp Val Val Gln Arg Leu Ser Ala Leu Gly  
 130 135 140

Leu Leu Val Ser Ile Thr Val Thr Ser Val Tyr Glu Ala Gly Val Ala  
 145 150 155 160

Ile Ala Ala Gly Ala Asp Ser Leu Val Val Gln Gly Pro Ala Ala Gly  
 165 170 175

Gly His Arg Gly Thr Phe Ala Pro Asp Met Glu Pro Gly Thr Glu Ser  
 180 185 190

Leu His Gln Leu Leu Asp Arg Ile Gly Ser Ala His Asp Val Pro Leu  
195 200 205

Val Ala Ala Gly Gly Leu Gly Thr Ala Glu Asp Val Ala Ala Val Leu  
210 215 220

Arg Arg Gly Ala Ile Ala Ala Gln Val Gly Thr Ala Leu Leu Leu Ala  
225 230 235 240

Asp Glu Ala Gly Thr Asn Ala Ala His Arg Ala Ala Leu Lys Asn Pro  
245 250 255

Glu Phe Asp Ala Thr Leu Val Thr Arg Ala Phe Ser Gly Arg Tyr Ala  
260 265 270

Arg Gly Leu Ala Asn Asn Phe Thr Arg Leu Leu Asp His Val Ala Pro  
275 280 285

Leu Gly Tyr Pro Glu Val His Gln Met Thr Lys Pro Ile Arg Ala Ala  
290 295 300

Ala Val Gln Ala Asp Asp Pro His Gly Thr Asn Leu Trp Ala Gly Ser  
305 310 315 320

Ala His Arg Lys Thr Arg Pro Gly Pro Ala Ala Asp Ile Ile Ala Ser  
325 330 335

Leu Thr Pro Asp Val Cys Ser Ala  
340

<210> 27

<211> 1068

<212> DNA

<213> Mycobacterium tuberculosis rv3553

<400> 27

atgaggctgc gtacgccgct gaccgagctc atcggcatcg agcaccgggt ggtgcagacc 60  
gggatgggct ggggtggccgg tgcccggtcg gtgtcggcga ccgccaacgc gggcgggctg 120  
ggcatcttgg cctcggccac catgacgctg gacgagctgg cggcggcgat cacaaaggtc 180  
aaggcgtca ccgacaagcc attcggggtg aacatccgcg ccgacgcagc cgacgcgggc 240  
gaccgcgtcg agttgatgat ccgcgagggg gtgcgggttg cctcggttcgc gttggcaccc 300  
aaacagcagc tgatcgcccg gctcaaagaa gccggcgcgg tggtcatacc gtcgatcggc 360  
gcggccaaac atgcgcgcaa ggtggcgggc tggggcgccg acgcgatgat cgtgcagggc 420

```

ggcgagggcg gcggccacac cgggccggtc gccaccacgc tgctgttgcc gtcgggtgctg 480
gacgccgtgg cgggcaccgg catcccgtg atcgccgcgc gcggcttctt cgacggggcg 540
gggctagccg cggcgttggt ctacggcgcc gccgggggtg ccatgggcac cgggtttctg 600
ctcacctcgg attccaccgt gcccgacgcg gtcaaacggc gttacctgca ggccggcttg 660
gacggcaccg tgggcaccac ccgcgtcgac gggatgccgc accgggtgct gcgcaccgag 720
ctggctgaga agctggaaaag cggctcgcg gcacgaggtt tcgcggccgc gctgcgcaat 780
gccggcaagt ttagacggat gtcgcagatg acctggcggt cgatgatccg agacggcctg 840
accatgcgcc acggcaagga attgacctgg tcacaggtgc tgatggcggc aaacaccccg 900
atgctgctca aagccggcct ggtcgacggc aacaccgagg ccgggggtgct ggcatcgggc 960
caggtagcgg gcattcttga cgacctaccg tcgtgcaaag agctgatcga gtcgatcggt 1020
cttgacgccca tcacacattt acaaaccgca tctgcgctgg tggagtga 1068

```

```

<210> 28
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis rv3553

```

```

<400> 28

```

```

Met Arg Leu Arg Thr Pro Leu Thr Glu Leu Ile Gly Ile Glu His Pro
1           5           10           15

```

```

Val Val Gln Thr Gly Met Gly Trp Val Ala Gly Ala Arg Leu Val Ser
          20           25           30

```

```

Ala Thr Ala Asn Ala Gly Gly Leu Gly Ile Leu Ala Ser Ala Thr Met
          35           40           45

```

```

Thr Leu Asp Glu Leu Ala Ala Ala Ile Thr Lys Val Lys Ala Val Thr
50           55           60

```

```

Asp Lys Pro Phe Gly Val Asn Ile Arg Ala Asp Ala Ala Asp Ala Gly
65           70           75           80

```

```

Asp Arg Val Glu Leu Met Ile Arg Glu Gly Val Arg Val Ala Ser Phe
          85           90           95

```

```

Ala Leu Ala Pro Lys Gln Gln Leu Ile Ala Arg Leu Lys Glu Ala Gly
100           105           110

```

```

Ala Val Val Ile Pro Ser Ile Gly Ala Ala Lys His Ala Arg Lys Val
115           120           125

```

Ala Ala Trp Gly Ala Asp Ala Met Ile Val Gln Gly Gly Glu Gly Gly  
130 135 140

Gly His Thr Gly Pro Val Ala Thr Thr Leu Leu Leu Pro Ser Val Leu  
145 150 155 160

Asp Ala Val Ala Gly Thr Gly Ile Pro Val Ile Ala Ala Gly Gly Phe  
165 170 175

Phe Asp Gly Arg Gly Leu Ala Ala Ala Leu Cys Tyr Gly Ala Ala Gly  
180 185 190

Val Ala Met Gly Thr Arg Phe Leu Leu Thr Ser Asp Ser Thr Val Pro  
195 200 205

Asp Ala Val Lys Arg Arg Tyr Leu Gln Ala Gly Leu Asp Gly Thr Val  
210 215 220

Val Thr Thr Arg Val Asp Gly Met Pro His Arg Val Leu Arg Thr Glu  
225 230 235 240

Leu Val Glu Lys Leu Glu Ser Gly Ser Arg Ala Arg Gly Phe Ala Ala  
245 250 255

Ala Leu Arg Asn Ala Gly Lys Phe Arg Arg Met Ser Gln Met Thr Trp  
260 265 270

Arg Ser Met Ile Arg Asp Gly Leu Thr Met Arg His Gly Lys Glu Leu  
275 280 285

Thr Trp Ser Gln Val Leu Met Ala Ala Asn Thr Pro Met Leu Leu Lys  
290 295 300

Ala Gly Leu Val Asp Gly Asn Thr Glu Ala Gly Val Leu Ala Ser Gly  
305 310 315 320

Gln Val Ala Gly Ile Leu Asp Asp Leu Pro Ser Cys Lys Glu Leu Ile  
325 330 335

Glu Ser Ile Val Leu Asp Ala Ile Thr His Leu Gln Thr Ala Ser Ala  
340 345 350

Leu Val Glu  
355

<210> 29  
 <211> 969  
 <212> DNA  
 <213> Mycobacterium tuberculosis rv0021c

```

<400> 29
gtggtgctat cgacggcctt tagccagatg ttcggaatcg actatccgat agtgtccgcg      60
ccaatggact tgatcgccgg cggtgagctg gctgccgcgg taagtggcgc agggggactc      120
ggcctcatcg ggggcggtta tggggaccgg gattggttg cccggcagtt cgatctcgcc      180
gctggagcgc cggtgggctg cgggttcac acctggtctt tggcccgcca accgcagctg      240
ctcgacctcg cgctgcagta tgagccggtg gcggtgatgc tgcgttcgg ggaccccgcg      300
gttttcgctg acgccatcaa gtccgccgga acgcggttg tctgccagat ccaaaaccgg      360
accaggccg agcgagccct gcaggtcggc gccgatgtgt tggaggctca gggcaccgag      420
gccggtgggc acggccacgg tccacgttcc accctgacct tggtagccga aatcgtcgac      480
ctggtcaccg cgcggggaac tgatatcccg gtgatcgccg ccgggggcat cgccgacggc      540
cggggccttg ccgccgcgtt gatgttggtt gccgccgggg tattggtcgg tacgcgcttc      600
tacgccacgg tcgaagcggt atccacaccg caggcgcggg acccgctgct ggcgggccact      660
ggcgacgaca tgtgccgcac cactatctac gatcagctac ggcgctatcc ctggccgcaa      720
ggacacacga tgagcgtgct aagcaacgcc ctccaccgac aattcgagga caccgaactc      780
gacattctcc atcgcaaga agccatggcc agatattggc gagccgttgc tgcgcgtgac      840
tacagcatcg ccaatgtcac cgccggtcaa gccgcggggc tggtaaatgc cgtcctgcca      900
gccgccgacg tgataaccgg tatggcgcaa caagcggcga ggacgctgac cgcgatgcgc      960
gcggtgtaa
  
```

<210> 30  
 <211> 322  
 <212> PRT  
 <213> Mycobacterium tuberculosis rv0021c

<400> 30

```

Met Val Leu Ser Thr Ala Phe Ser Gln Met Phe Gly Ile Asp Tyr Pro
1           5           10           15
  
```

```

Ile Val Ser Ala Pro Met Asp Leu Ile Ala Gly Gly Glu Leu Ala Ala
          20           25           30
  
```

```

Ala Val Ser Gly Ala Gly Gly Leu Gly Leu Ile Gly Gly Gly Tyr Gly
          35           40           45
  
```



Asp Arg Asp Trp Leu Ala Arg Gln Phe Asp Leu Ala Ala Gly Ala Pro  
50 55 60

Val Gly Cys Gly Phe Ile Thr Trp Ser Leu Ala Arg Gln Pro Gln Leu  
65 70 75 80

Leu Asp Leu Ala Leu Gln Tyr Glu Pro Val Ala Val Met Leu Ser Phe  
85 90 95

Gly Asp Pro Ala Val Phe Ala Asp Ala Ile Lys Ser Ala Gly Thr Arg  
100 105 110

Leu Val Cys Gln Ile Gln Asn Arg Thr Gln Ala Glu Arg Ala Leu Gln  
115 120 125

Val Gly Ala Asp Val Leu Val Ala Gln Gly Thr Glu Ala Gly Gly His  
130 135 140

Gly His Gly Pro Arg Ser Thr Leu Thr Leu Val Pro Glu Ile Val Asp  
145 150 155 160

Leu Val Thr Ala Arg Gly Thr Asp Ile Pro Val Ile Ala Ala Gly Gly  
165 170 175

Ile Ala Asp Gly Arg Gly Leu Ala Ala Ala Leu Met Leu Gly Ala Ala  
180 185 190

Gly Val Leu Val Gly Thr Arg Phe Tyr Ala Thr Val Glu Ala Leu Ser  
195 200 205

Thr Pro Gln Ala Arg Asp Pro Leu Leu Ala Ala Thr Gly Asp Asp Met  
210 215 220

Cys Arg Thr Thr Ile Tyr Asp Gln Leu Arg Arg Tyr Pro Trp Pro Gln  
225 230 235 240

Gly His Thr Met Ser Val Leu Ser Asn Ala Leu Thr Asp Gln Phe Glu  
245 250 255

Asp Thr Glu Leu Asp Ile Leu His Arg Glu Glu Ala Met Ala Arg Tyr  
260 265 270

Trp Arg Ala Val Ala Ala Arg Asp Tyr Ser Ile Ala Asn Val Thr Ala  
275 280 285

Gly Gln Ala Ala Gly Leu Val Asn Ala Val Leu Pro Ala Ala Asp Val

290

295

300

Ile Thr Gly Met Ala Gln Gln Ala Ala Arg Thr Leu Thr Ala Met Arg  
 305 310 315 320

Ala Val

<210> 31  
 <211> 1131  
 <212> DNA  
 <213> Mycobacterium tuberculosis rv1894c

<400> 31  
 atgcacactg ccatttgcca cgagctcggt atcgagtttc ctatttttgc cttcactcac 60  
 tgccgcgatg tgggtggcgc cgtcagcaaa gctgggtggtt ttggtgtgct cggagcagtt 120  
 ggggttcacgc cggagcagct ggagatcgag ctcaactgga tcgatgaaca catcggcgac 180  
 caccctacg gggtcgacat cgtgatcccg aacaagtacg agggcatgga ctcccagctg 240  
 tcggcggatg agctcgccaa gacgctgcgg tcgatgggtcc cgcaggagca tctggacttc 300  
 gcccgcaaga tcctcgccga tcatgggtgtc ccggtcgagg acgccgacga ggacagtctg 360  
 cagctgctcg gttggaccga ggcgacggcc accccacagg tcgacgcggc gctgaagcac 420  
 cccaagatga cgatggtcgc caacgcgctt ggcaccccc cagcggacat gatcaagcac 480  
 atccacgact cgggtcgcaa ggtggccgca ttgtgcggt caccctcgca ggcccgcaag 540  
 cagcgcgatg cgggcgtcga catcatcatc gccagggcg gcgaggccgg cgggcactgt 600  
 ggcgaggtgg gctccattgt gttgtggcct caggctgtca aggaggtagc gccggttcgg 660  
 gtgttggcgg cgggtggcat cggcagcggc cagcagatcg ctgcagcgtt ggcgctgggg 720  
 acccaagggg catggaccgg ttgcagtggt ctgatggtcg aggaagccgc aaacaccgcg 780  
 gttcaacagg ccgcatacgt caaggcgacc agccgcgaca ccgtgcgcag tcgttccttc 840  
 acgggtaagc cggcccggat gctgcgcaac gactggactg aggcctggga gcaaccggag 900  
 agcccgaagc cgctcggtat gccgttgcaa tacatggtct ccggcatggc cgtcaaagcc 960  
 acacataaat acccgaacga gaccgtcgac gtcgcgttca acccgggtggg gcaggttggt 1020  
 gggcagttca ccaaggtgga aaagacggct accgttatcg aacgctgggt gcaggagtac 1080  
 ctcgaggcga ccgcccgggt ggacgcactc aatgctgccg cgtccgtttg a 1131

<210> 32  
 <211> 376  
 <212> PRT  
 <213> Mycobacterium tuberculosis rv1894c

&lt;400&gt; 32

Met His Thr Ala Ile Cys Asp Glu Leu Gly Ile Glu Phe Pro Ile Phe  
1 5 10 15

Ala Phe Thr His Cys Arg Asp Val Val Val Ala Val Ser Lys Ala Gly  
20 25 30

Gly Phe Gly Val Leu Gly Ala Val Gly Phe Thr Pro Glu Gln Leu Glu  
35 40 45

Ile Glu Leu Asn Trp Ile Asp Glu His Ile Gly Asp His Pro Tyr Gly  
50 55 60

Val Asp Ile Val Ile Pro Asn Lys Tyr Glu Gly Met Asp Ser Gln Leu  
65 70 75 80

Ser Ala Asp Glu Leu Ala Lys Thr Leu Arg Ser Met Val Pro Gln Glu  
85 90 95

His Leu Asp Phe Ala Arg Lys Ile Leu Ala Asp His Gly Val Pro Val  
100 105 110

Glu Asp Ala Asp Glu Asp Ser Leu Gln Leu Leu Gly Trp Thr Glu Ala  
115 120 125

Thr Ala Thr Pro Gln Val Asp Ala Ala Leu Lys His Pro Lys Met Thr  
130 135 140

Met Val Ala Asn Ala Leu Gly Thr Pro Pro Ala Asp Met Ile Lys His  
145 150 155 160

Ile His Asp Ser Gly Arg Lys Val Ala Ala Leu Cys Gly Ser Pro Ser  
165 170 175

Gln Ala Arg Lys His Ala Asp Ala Gly Val Asp Ile Ile Ile Ala Gln  
180 185 190

Gly Gly Glu Ala Gly Gly His Cys Gly Glu Val Gly Ser Ile Val Leu  
195 200 205

Trp Pro Gln Val Val Lys Glu Val Ala Pro Val Pro Val Leu Ala Ala  
210 215 220

Gly Gly Ile Gly Ser Gly Gln Gln Ile Ala Ala Ala Leu Ala Leu Gly  
225 230 235 240

Thr Gln Gly Ala Trp Thr Gly Ser Gln Trp Leu Met Val Glu Glu Ala  
245 250 255

Ala Asn Thr Ala Val Gln Gln Ala Ala Tyr Val Lys Ala Thr Ser Arg  
260 265 270

Asp Thr Val Arg Ser Arg Ser Phe Thr Gly Lys Pro Ala Arg Met Leu  
275 280 285

Arg Asn Asp Trp Thr Glu Ala Trp Glu Gln Pro Glu Ser Pro Lys Pro  
290 295 300

Leu Gly Met Pro Leu Gln Tyr Met Val Ser Gly Met Ala Val Lys Ala  
305 310 315 320

Thr His Lys Tyr Pro Asn Glu Thr Val Asp Val Ala Phe Asn Pro Val  
325 330 335

Gly Gln Val Val Gly Gln Phe Thr Lys Val Glu Lys Thr Ala Thr Val  
340 345 350

Ile Glu Arg Trp Val Gln Glu Tyr Leu Glu Ala Thr Ala Arg Leu Asp  
355 360 365

Ala Leu Asn Ala Ala Ala Ser Val  
370 375

<210> 33  
<211> 945  
<212> DNA  
<213> Thermotoga maritima

<400> 33  
atgaccgtga gaacaagagt gacagatctt ctggaaatag agcatccaat cctcatgggt 60  
ggaatggcct gggcggaac tcccaccctc gcagcagcgg tatcggaggc gggaggactt 120  
ggaatcatcg gatccggagc catgaagccg gacgacctga gaaaagcgat ctccgaactc 180  
agacagaaga cggacaaacc cttcggtgta aacataatcc ttgtctctcc gtgggaggac 240  
gatctcgtca aggtgtgcat agaagagaaa gtaccgctcg tcacgttcgg tgcgggaaac 300  
ccaacgaagt acataaggga actcaaggaa aacggaacaa aggtgatacc cgttgtcgcc 360  
tccgactctc tggcaaggat ggtggaaaga gcgggagcgg atgcggtgat agcggaaggg 420  
atggagtcg gtggacacat aggtgaagtc acaaccttcg ttctcgtcaa caaagtctcc 480  
aggagtgtga acatccccgt gatcgagcgg ggaggcatcg ccgacggaag aggtatggca 540

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gccgccttcg cactcggagc ggaagccgtt cagatgggaa ccaggtttgt ggcgagtgtg      600
gaaagcgacg tgcacccggt ttacaaagaa aagatcgta aggcttccat aagagacacc      660
gttgtgacgg gagccaaact tggacacccc gcgcgcgttc tcagaactcc ctttgcaagg      720
aagatccagg agatggagtt tgaaaacccc atgcaggctg aagaaatgct ggtgggaagt      780
ctcagaagag cggtcgttga aggcgatctg gagagaggat ccttcatggt gggacagagc      840
gccggccttga tcgatgagat aaaaccggtg aagcagatca tagaggatat cctgaaggag      900
ttcaaagaaa cgggtggagaa gctgaggggg tacatcgaag agtga                      945

```

```

<210> 34
<211> 314
<212> PRT
<213> Thermotoga maritima

```

```

<400> 34

```

```

Met Thr Val Arg Thr Arg Val Thr Asp Leu Leu Glu Ile Glu His Pro
1              5              10              15

```

```

Ile Leu Met Gly Gly Met Ala Trp Ala Gly Thr Pro Thr Leu Ala Ala
20              25              30

```

```

Ala Val Ser Glu Ala Gly Gly Leu Gly Ile Ile Gly Ser Gly Ala Met
35              40              45

```

```

Lys Pro Asp Asp Leu Arg Lys Ala Ile Ser Glu Leu Arg Gln Lys Thr
50              55              60

```

```

Asp Lys Pro Phe Gly Val Asn Ile Ile Leu Val Ser Pro Trp Ala Asp
65              70              75              80

```

```

Asp Leu Val Lys Val Cys Ile Glu Glu Lys Val Pro Val Val Thr Phe
85              90              95

```

```

Gly Ala Gly Asn Pro Thr Lys Tyr Ile Arg Glu Leu Lys Glu Asn Gly
100             105             110

```

```

Thr Lys Val Ile Pro Val Val Ala Ser Asp Ser Leu Ala Arg Met Val
115             120             125

```

```

Glu Arg Ala Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ser Gly
130             135             140

```

```

Gly His Ile Gly Glu Val Thr Thr Phe Val Leu Val Asn Lys Val Ser
145             150             155             160

```

Arg Ser Val Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly  
165 170 175

Arg Gly Met Ala Ala Ala Phe Ala Leu Gly Ala Glu Ala Val Gln Met  
180 185 190

Gly Thr Arg Phe Val Ala Ser Val Glu Ser Asp Val His Pro Val Tyr  
195 200 205

Lys Glu Lys Ile Val Lys Ala Ser Ile Arg Asp Thr Val Val Thr Gly  
210 215 220

Ala Lys Leu Gly His Pro Ala Arg Val Leu Arg Thr Pro Phe Ala Arg  
225 230 235 240

Lys Ile Gln Glu Met Glu Phe Glu Asn Pro Met Gln Ala Glu Glu Met  
245 250 255

Leu Val Gly Ser Leu Arg Arg Ala Val Val Glu Gly Asp Leu Glu Arg  
260 265 270

Gly Ser Phe Met Val Gly Gln Ser Ala Gly Leu Ile Asp Glu Ile Lys  
275 280 285

Pro Val Lys Gln Ile Ile Glu Asp Ile Leu Lys Glu Phe Lys Glu Thr  
290 295 300

Val Glu Lys Leu Arg Gly Tyr Ile Glu Glu  
305 310

<210> 35

<211> 1092

<212> DNA

<213> Helicobacter pylori

<400> 35

atggtatcaa cactcaaacc gctaaaaatc ggtaaacaca ccataaaatt ccoctatTTTT 60  
caaggggggca tgggtgtggg gattagctgg gatgaactag ctggaaatgt tgccaaagaa 120  
ggggcctttag gagtgatttc agccgtaggg actggttatt ataaaaacat gcgttttgta 180  
gaaaggattg tggctaaaaa accctttgaa gccttgaatt tttactccaa aaaagcgttg 240  
aatgagattt ttgcaaacgc taggaaaatt tgcgggaaca agcctttggg ggccaatatt 300  
ttatacgcta tcaatgacta tggccgtgtt ttaagggaact cttgtgaggc gggggcgaa 360  
attatcatta caggggctgg ttgcccact aacatgcctg aattcgctaa ggatttttagc 420

```

gatgtggcgc tcatccctat catttcctca gcgaaggctt taaaaatcct ttgtaaaaga 480
tggagcgatc gctataaaag aatcccggac gcattcattg tggaagggcc ttgagtgagg 540
gggcatcagg gcttttaaata cgaagattgt ttcaaagaag aattccaatt agaaaactta 600
gtgcctaaag tcgtggaagc ttctaaagaa tgggggaata tccctatcat cgccgcgggg 660
gggatttggg ataagaaaga tatagacacc atgttaagcc ttggagcgag tggggtgcaa 720
atggcgactc gtttttttagg cacgaaagaa tgcgacgcta aagcgtatgc cgatcttttg 780
cccacgctca aaaaagaaga tattttactc atcaaatcgc ctgtaggcta tccggctagg 840
gctatcaata cgggggtgat caaacgcatt gaagagggtta acgcgcctaa aatcgcatgc 900
gtgagcaatt gtgtagcgcc ttgtaacagg ggtgaagaag ctaaaaaggt gggctattgt 960
atcgctgatg gtttggggcg cagttattta ggaaacagag aagaggggct ttattttacc 1020
ggggctaatz gctatagagt ggataagatt atcagcgtgc atgaattgat taaagagctt 1080
acagagggtt aa 1092

```

```

<210> 36
<211> 363
<212> PRT
<213> Helicobacter pylori

```

```

<400> 36

```

```

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
1          5          10          15

```

```

Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
20          25          30

```

```

Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
35          40          45

```

```

Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
50          55          60

```

```

Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
65          70          75          80

```

```

Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu
85          90          95

```

```

Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg
100          105          110

```

```

Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu

```

115

120

125

Pro Thr Asn Met Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu  
 130 135 140

Ile Pro Ile Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg  
 145 150 155 160

Trp Ser Asp Arg Tyr Lys Arg Ile Pro Asp Ala Phe Ile Val Glu Gly  
 165 170 175

Pro Leu Ser Gly Gly His Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys  
 180 185 190

Glu Glu Phe Gln Leu Glu Asn Leu Val Pro Lys Val Val Glu Ala Ser  
 195 200 205

Lys Glu Trp Gly Asn Ile Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp  
 210 215 220

Lys Lys Asp Ile Asp Thr Met Leu Ser Leu Gly Ala Ser Gly Val Gln  
 225 230 235 240

Met Ala Thr Arg Phe Leu Gly Thr Lys Glu Cys Asp Ala Lys Ala Tyr  
 245 250 255

Ala Asp Leu Leu Pro Thr Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys  
 260 265 270

Ser Pro Val Gly Tyr Pro Ala Arg Ala Ile Asn Thr Gly Val Ile Lys  
 275 280 285

Arg Ile Glu Glu Gly Asn Ala Pro Lys Ile Ala Cys Val Ser Asn Cys  
 290 295 300

Val Ala Pro Cys Asn Arg Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys  
 305 310 315 320

Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly  
 325 330 335

Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser  
 340 345 350

Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly  
 355 360



<210> 37  
 <211> 825  
 <212> DNA  
 <213> Archaeoglobus fulgidus

<400> 37  
 atgaacagga ttgctaaact cctcaaaacg aagtatccga tagttcaggg cccgatggcc 60  
 ggaataactc tcggagaatt tgcttctaca gtgtctgagg ctggcgggct tggagttata 120  
 gcttctgccc gcctttcgcc tgaaaaacta aaagaggaga tagagaaagt taagaacagg 180  
 actgataagc ccttcgccgt gaacattcca atatatcagc cgggctcgga gaagaatctt 240  
 gagactgcac ttaaagctga tgttgggatt atttacacct ctgcaggaag cccggagaaa 300  
 tacactgaga gagtaaagga atccggggca aaagtcatac acaaggtgtc gaggttgaaa 360  
 gaggggctga aagcggagaa ggcgggagtg gatgctgtgg ttgcgatggg ctttgaggcg 420  
 ggagggatta tagggaggag tgggtgaaca tccttctgct tgattcctga gcttgccgac 480  
 aacctcagca ttccagttgt agccgctggc gggatagcag atgagagggg atttgctgca 540  
 gccctgattc tcggagcgga aggtgttgag attggcacga gactgcttgc aaccaaagag 600  
 tgtcccgctgc cggaaagcat taagcaagct attttaaaag ccacctgcga ctccacgatg 660  
 gttattgaga gcccggttgt aatgagagct ctcaagccag agctgagcgg agattctgag 720  
 aatcctgctc tgggagggca ggtttcaggg ctgattaagg agattcttac ggttgaagag 780  
 gtaatcagga aaattgcaga ggggctgaat aaagctaaat tctaa 825

<210> 38  
 <211> 274  
 <212> PRT  
 <213> Archaeoglobus fulgidus

<400> 38

Met Asn Arg Ile Ala Lys Leu Leu Lys Thr Lys Tyr Pro Ile Val Gln  
 1 5 10 15

Gly Pro Met Ala Gly Ile Thr Leu Gly Glu Phe Ala Ser Thr Val Ser  
 20 25 30

Glu Ala Gly Gly Leu Gly Val Ile Ala Ser Ala Gly Leu Ser Pro Glu  
 35 40 45

Lys Leu Lys Glu Glu Ile Glu Lys Val Lys Asn Arg Thr Asp Lys Pro  
 50 55 60

Phe Ala Val Asn Ile Pro Ile Tyr Gln Pro Gly Ser Glu Lys Asn Leu

65		70		75		80
Glu Thr Ala Leu Lys Ala Asp Val Gly Ile Ile Tyr Thr Ser Ala Gly	85		90		95	
Ser Pro Glu Lys Tyr Thr Glu Arg Val Lys Glu Ser Gly Ala Lys Val	100		105		110	
Ile His Lys Val Ser Arg Leu Lys Glu Gly Leu Lys Ala Glu Lys Ala	115		120		125	
Gly Val Asp Ala Val Val Ala Met Gly Phe Glu Ala Gly Gly Ile Ile	130		135		140	
Gly Arg Ser Gly Val Thr Ser Phe Cys Leu Ile Pro Glu Leu Ala Asp	145		150		155	160
Asn Leu Ser Ile Pro Val Val Ala Ala Gly Gly Ile Ala Asp Glu Arg	165		170		175	
Gly Phe Ala Ala Ala Leu Ile Leu Gly Ala Glu Gly Val Glu Ile Gly	180		185		190	
Thr Arg Leu Leu Ala Thr Lys Glu Cys Pro Val Pro Glu Ser Ile Lys	195		200		205	
Gln Ala Ile Leu Lys Ala Thr Cys Asp Ser Thr Met Val Ile Glu Ser	210		215		220	
Pro Val Val Met Arg Ala Leu Lys Pro Glu Leu Ser Gly Asp Ser Glu	225		230		235	240
Asn Pro Ala Leu Gly Gly Gln Val Ser Gly Leu Ile Lys Glu Ile Leu	245		250		255	
Thr Val Glu Glu Val Ile Arg Lys Ile Ala Glu Gly Leu Asn Lys Ala	260		265		270	

Lys Phe

<210> 39  
 <211> 1125  
 <212> DNA  
 <213> Williopsis saturnus  
 <400> 39

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attgggttoga tccctatggg ctcgctgagt gagaagtgtg atgctattga gacccagctg      180
gaaaattttg atgaattggg tgggtattct ggaaggatag tcaacttgaa cttctttgct      240
cataaggagc ctcgttctgg gagagctgat gtcaacgagg aatgggtcaa gaagtatgac      300
aagatatatg gcaaagccgg aattgagttt gacaaaaagg agctgaagtt gttatatcca      360
tcttttaggt ccattgttga tccacaacat ccgactgtgc ggctactgaa gaatctcaag      420
ccaaagattg tcagttttcca ctttgggtta ccccatgagg cgggtattga atctctccag      480
gcaagcgata ttaagatctt tgtcactgtc acaaactctac aggagtttca gcaggcttat      540
gagtctaaat tggatgggtg cgtcctacaa ggatgggaag ctgggtggaca tcgtggtaat      600
ttcaaggcta atgacgtcga agatgggaaa ctgaagacgt tggatctcgt tagtactatt      660
gttgattaca ttgactcggc tagtatctcc aatccaccat ttatcattgc agcgggtggg      720
attcatgatg atgagtccat caaagaattg cttcaattca acattgctgc cgttcagttg      780
ggtagtgttt gggttaccatc gagccaggcc acaatatctc ctgaacattt gaagatgttt      840
caatccccaa aaagtgcac gatgatgacc gcagccattt caggacgtaa cttgagaacg      900
atcagtacac ctttcttgag ggatcttcat caatcttcac cattggcctc gatccctgat      960
tatccattac cttacgacag ctttaagtca cttgctaatt acgctaagca aagtggaaaa      1020
gggcctcagt actccgcatt tcttgctgga tctaactatc acaaactctg gaaggatacg      1080
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<210> 40
<211> 374
<212> PRT
<213> Williopsis saturnus

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<400> 40
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Met Arg Ser Gln Ile Gln Ser Phe Leu Lys Thr Phe Glu Val Arg Tyr
1           5           10          15

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Pro Ile Ile Gln Ala Pro Met Ala Gly Ala Ser Thr Leu Glu Leu Ala
          20          25          30

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Ala Thr Val Thr Arg Leu Gly Gly Ile Gly Ser Ile Pro Met Gly Ser
          35          40          45

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Leu Ser Glu Lys Cys Asp Ala Ile Glu Thr Gln Leu Glu Asn Phe Asp
          50          55          60

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Glu Leu Val Gly Asp Ser Gly Arg Ile Val Asn Leu Asn Phe Phe Ala  
65 70 75 80

His Lys Glu Pro Arg Ser Gly Arg Ala Asp Val Asn Glu Glu Trp Leu  
85 90 95

Lys Lys Tyr Asp Lys Ile Tyr Gly Lys Ala Gly Ile Glu Phe Asp Lys  
100 105 110

Lys Glu Leu Lys Leu Leu Tyr Pro Ser Phe Arg Ser Ile Val Asp Pro  
115 120 125

Gln His Pro Thr Val Arg Leu Leu Lys Asn Leu Lys Pro Lys Ile Val  
130 135 140

Ser Phe His Phe Gly Leu Pro His Glu Ala Val Ile Glu Ser Leu Gln  
145 150 155 160

Ala Ser Asp Ile Lys Ile Phe Val Thr Val Thr Asn Leu Gln Glu Phe  
165 170 175

Gln Gln Ala Tyr Glu Ser Lys Leu Asp Gly Val Val Leu Gln Gly Trp  
180 185 190

Glu Ala Gly Gly His Arg Gly Asn Phe Lys Ala Asn Asp Val Glu Asp  
195 200 205

Gly Gln Leu Lys Thr Leu Asp Leu Val Ser Thr Ile Val Asp Tyr Ile  
210 215 220

Asp Ser Ala Ser Ile Ser Asn Pro Pro Phe Ile Ile Ala Ala Gly Gly  
225 230 235 240

Ile His Asp Asp Glu Ser Ile Lys Glu Leu Leu Gln Phe Asn Ile Ala  
245 250 255

Ala Val Gln Leu Gly Thr Val Trp Leu Pro Ser Ser Gln Ala Thr Ile  
260 265 270

Ser Pro Glu His Leu Lys Met Phe Gln Ser Pro Lys Ser Asp Thr Met  
275 280 285

Met Thr Ala Ala Ile Ser Gly Arg Asn Leu Arg Thr Ile Ser Thr Pro  
290 295 300

Phe Leu Arg Asp Leu His Gln Ser Ser Pro Leu Ala Ser Ile Pro Asp  
 305 310 315 320

Tyr Pro Leu Pro Tyr Asp Ser Phe Lys Ser Leu Ala Asn Asp Ala Lys  
 325 330 335

Gln Ser Gly Lys Gly Pro Gln Tyr Ser Ala Phe Leu Ala Gly Ser Asn  
 340 345 350

Tyr His Lys Ser Trp Lys Asp Thr Arg Ser Thr Glu Glu Ile Phe Ser  
 355 360 365

Ile Leu Val Gln Asp Leu  
 370

<210> 41  
 <211> 1215  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 41  
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 cctatggcgg gggtcacgac tattgaaatg gccgctaagg cttgtattgc gggcgccata 180  
 gcttcactac ccctatccca cttagacttc agaaagggtca atgatattga aaagcttaaa 240  
 ctgatggttt cacaattcag agatcaagta gccgatgaat ctttagaggg caatctcaac 300  
 ctaaactttt ttgccatga tatcgttgat aaaccgaccg atcttcaaac agctaactgg 360  
 gcgaagctat acagaaagtc tatgaatgtg ccgattgata tgaatgagat taaattcgat 420  
 aatggtaatg tatcttttaa ggcatttgaa aaagaaaatg ctcttcaaga ttttttccag 480  
 tacctatcag atggcttttag gcctaaaatc attagtttcc attttggcca tccgtcgaaa 540  
 tctacaatag aatatttaca aaaaattgga attctaattt ttgtgactgc cacctctgta 600  
 agagaagttc gattgttagc acgtctcggc attaattggca tagtgtgtca aggctatgaa 660  
 gcgggaggac atagaggaaa tttcttagta aatgaccca aagatgatga aaacttatca 720  
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 atacatgcta ctccctttgt cattgcagca ggtgggtataa tggattcaa agatatatca 840  
 tacatgttat cacagcaagc agacgtctgt caagtgggga ctgcttttct tggttgcagt 900  
 gaatccaatg catcaaaaaa cttttcaagc cccttcactc gagaaacaac aactaaaatg 960  
 gttaatataa tatcaggaaa gcctgcaagg accatctcta ctctttttat cgaaaaagtc 1020  
 attgctaatt ttcaagggtga ggagcttctt ccatatggct acatgtatag tgctttcaag 1080

caagtaagaa aaaagtatcc agaattggct aactttattt tagctggaca aggatttcag 1140  
aatgtccaat caggaatcac aacagacaag aaaattgaaa ctatgggcgc aagattgaaa 1200  
attgtcgga aataa 1215

<210> 42  
<211> 404  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 42

Met Tyr Phe Leu Asn Gln Leu Ile Phe Gln Asp Val Ser Val Met Ser  
1 5 10 15

Val Asp Lys Arg Glu Asp Met Ser Arg Ser Phe Gln Lys Cys Leu Asn  
20 25 30

Leu Arg Tyr Pro Ile Ile Gln Ala Pro Met Ala Gly Val Thr Thr Ile  
35 40 45

Glu Met Ala Ala Lys Ala Cys Ile Ala Gly Ala Ile Ala Ser Leu Pro  
50 55 60

Leu Ser His Leu Asp Phe Arg Lys Val Asn Asp Ile Glu Lys Leu Lys  
65 70 75 80

Leu Met Val Ser Gln Phe Arg Asp Gln Val Ala Asp Glu Ser Leu Glu  
85 90 95

Gly Asn Leu Asn Leu Asn Phe Phe Cys His Asp Ile Val Asp Lys Pro  
100 105 110

Thr Asp Leu Gln Thr Ala Asn Trp Ala Lys Leu Tyr Arg Lys Ser Met  
115 120 125

Asn Val Pro Ile Asp Met Asn Glu Ile Lys Phe Asp Asn Gly Asn Val  
130 135 140

Ser Phe Lys Ala Phe Glu Lys Glu Asn Ala Leu Gln Asp Phe Phe Gln  
145 150 155 160

Tyr Leu Ser Asp Gly Phe Arg Pro Lys Ile Ile Ser Phe His Phe Gly  
165 170 175

His Pro Ser Lys Ser Thr Ile Glu Tyr Leu Gln Lys Ile Gly Ile Leu  
180 185 190

Ile Phe Val Thr Ala Thr Ser Val Arg Glu Val Arg Leu Leu Ala Arg  
 195 200 205

Leu Gly Ile Asn Gly Ile Val Cys Gln Gly Tyr Glu Ala Gly Gly His  
 210 215 220

Arg Gly Asn Phe Leu Val Asn Asp Pro Lys Asp Asp Glu Asn Leu Ser  
 225 230 235 240

Thr Val Gln Leu Val Lys Arg Thr Val Asp Glu Leu Ala Glu Met Lys  
 245 250 255

Asn Lys Gly Leu Ile His Ala Thr Pro Phe Val Ile Ala Ala Gly Gly  
 260 265 270

Ile Met Asp Ser Lys Asp Ile Ser Tyr Met Leu Ser Gln Gln Ala Asp  
 275 280 285

Ala Val Gln Val Gly Thr Ala Phe Leu Gly Cys Ser Glu Ser Asn Ala  
 290 295 300

Ser Lys Asn Phe Ser Ser Pro Phe Thr Arg Glu Thr Thr Thr Lys Met  
 305 310 315 320

Val Asn Ile Ile Ser Gly Lys Pro Ala Arg Thr Ile Ser Thr Pro Phe  
 325 330 335

Ile Glu Lys Val Ile Ala Asn Phe Gln Gly Glu Glu Leu Pro Pro Tyr  
 340 345 350

Gly Tyr Met Tyr Ser Ala Phe Lys Gln Val Arg Lys Lys Tyr Pro Glu  
 355 360 365

Leu Ala Asn Phe Ile Leu Ala Gly Gln Gly Phe Gln Asn Val Gln Ser  
 370 375 380

Gly Ile Thr Thr Asp Lys Lys Ile Glu Thr Met Gly Ala Arg Leu Lys  
 385 390 395 400

Ile Val Gly Lys

<210> 43  
 <211> 1137  
 <212> DNA

<213> *Neurospora crassa*

<400> 43

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atcgccaacg gcactcttgc ggccgaggtta tccaaggccg gcggtattgg ctttgtcgcc      180
ggcgggtccg acttcgcgcc cggctcctcc cacctaaccg cctctcttac cgaactcgcc      240
tccgcccgcg gcgcctcggg tcttaccgac cgccccctca cccctctccc cggcattggc      300
gtcggcctca ttttaaccca caccatctcc gttccctacg taaccgacac cgtcctgccc      360
atcctgatcg aacactcccc gcaagcagtc tggctcttcg ccaacgaccc ggatttcgag      420
gcctcttccg agcctggcgc aaagggaaca gcaaagcaaa tcatcgaggc ccttcacgct      480
tcgggggttcg tgggtattctt tcaagtaggc acggtgaaag atgcaaggaa ggcggcggca      540
gatggggcag atgtgattgt tgcgcaaggg atcgatgcgg gagggcatca gcttgctaca      600
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gaacgagagg tgggtggtgtt ggcggcggga ggtgtggcgg atgggagggg ggttgtaggg      720
gcgctgggtc tagggcgccg ggggtgtggt ttgggtacta gggtcaccgt agcagtcgaa      780
gcttccaccc ccgagttccg caggaaggtc atcctcgaga caaacgatgg tggtctcaac      840
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gacgggcgag ccgttcgcaa tgcctcctac gacgaccacg cggccggtgt cccctttgaa      960
gagaatcaca agaagttcaa ggaggcagcg agctctgggg ataactcgcg ggctgtgact     1020
tggtccggga ctgctgtggg tctgataaag gaccagaggc cggctggcga tattgttagg     1080
gagttgaggg aagaggccaa agagaggatc aagaagattc aggcttttgc tgcttaa      1137

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<210> 44

<211> 378

<212> PRT

<213> *Neurospora crassa*

<400> 44

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Met His Phe Pro Gly His Ser Ser Lys Lys Glu Glu Ser Ala Gln Ala
1              5              10              15

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Ala Leu Thr Lys Leu Asn Ser Trp Phe Pro Thr Thr Lys Asn Pro Val
              20              25              30

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Ile Ile Ser Ala Pro Met Tyr Leu Ile Ala Asn Gly Thr Leu Ala Ala
              35              40              45

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Glu Val Ser Lys Ala Gly Gly Ile Gly Phe Val Ala Gly Gly Ser Asp  
 50 55 60

Phe Arg Pro Gly Ser Ser His Leu Thr Ala Leu Ser Thr Glu Leu Ala  
 65 70 75 80

Ser Ala Arg Ser Arg Leu Gly Leu Thr Asp Arg Pro Leu Thr Pro Leu  
 85 90 95

Pro Gly Ile Gly Val Gly Leu Ile Leu Thr His Thr Ile Ser Val Pro  
 100 105 110

Tyr Val Thr Asp Thr Val Leu Pro Ile Leu Ile Glu His Ser Pro Gln  
 115 120 125

Ala Val Trp Leu Phe Ala Asn Asp Pro Asp Phe Glu Ala Ser Ser Glu  
 130 135 140

Pro Gly Ala Lys Gly Thr Ala Lys Gln Ile Ile Glu Ala Leu His Ala  
 145 150 155 160

Ser Gly Phe Val Val Phe Phe Gln Val Gly Thr Val Lys Asp Ala Arg  
 165 170 175

Lys Ala Ala Ala Asp Gly Ala Asp Val Ile Val Ala Gln Gly Ile Asp  
 180 185 190

Ala Gly Gly His Gln Leu Ala Thr Gly Ser Gly Ile Val Ser Leu Val  
 195 200 205

Pro Glu Val Arg Asp Met Leu Asp Arg Glu Phe Lys Glu Arg Glu Val  
 210 215 220

Val Val Val Ala Ala Gly Gly Val Ala Asp Gly Arg Gly Val Val Gly  
 225 230 235 240

Ala Leu Gly Leu Gly Ala Glu Gly Val Val Leu Gly Thr Arg Phe Thr  
 245 250 255

Val Ala Val Glu Ala Ser Thr Pro Glu Phe Arg Arg Lys Val Ile Leu  
 260 265 270

Glu Thr Asn Asp Gly Gly Leu Asn Thr Val Lys Ser His Phe His Asp  
 275 280 285

Gln Ile Asn Cys Asn Thr Ile Trp His Asn Val Tyr Asp Gly Arg Ala

290

295

300

Val Arg Asn Ala Ser Tyr Asp Asp His Ala Ala Gly Val Pro Phe Glu  
 305 310 315 320

Glu Asn His Lys Lys Phe Lys Glu Ala Ala Ser Ser Gly Asp Asn Ser  
 325 330 335

Arg Ala Val Thr Trp Ser Gly Thr Ala Val Gly Leu Ile Lys Asp Gln  
 340 345 350

Arg Pro Ala Gly Asp Ile Val Arg Glu Leu Arg Glu Glu Ala Lys Glu  
 355 360 365

Arg Ile Lys Lys Ile Gln Ala Phe Ala Ala  
 370 375

<210> 45

<211> 195

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabK Consensus Sequence

<220>

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<222> (2)..(2)

<223> X=Ile or Ala

<220>

<221> MISC\_FEATURE

<222> (3)..(4)

<223> X=any amino acid

<220>

<221> MISC\_FEATURE

<222> (5)..(5)

<223> X=Gly or Ala

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> X=Gly or Pro

<220>

<221> MISC\_FEATURE

<222> (8)..(16)

<223> X=any amino acid and up to 3 may be absent

<220>  
<221> MISC\_FEATURE  
<222> (18)..(19)  
<223> X=Pro, Ala, Gly, Ser or Thr

<220>  
<221> MISC\_FEATURE  
<222> (21)..(21)  
<223> X=Ser or Ala

<220>  
<221> MISC\_FEATURE  
<222> (22)..(23)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (26)..(53)  
<223> X=any amino acid and up to 6 may be absent

<220>  
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<222> (55)..(55)  
<223> X=Gln, Asn, Glu or Asp

<220>  
<221> MISC\_FEATURE  
<222> (56)..(56)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (59)..(59)  
<223> X=Gly or Ala

<220>  
<221> MISC\_FEATURE  
<222> (61)..(165)  
<223> X=any amino acid and up to 15 may be absent

<220>  
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<222> (167)..(168)  
<223> X=Ile or Val

<220>  
<221> MISC\_FEATURE  
<222> (169)..(169)  
<223> X=Ala or Gly

<220>



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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
                   115                                  120                                  125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
                   130                                  135                                  140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
                   145                                  150                                  155                                  160

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa  
                                   165                                  170                                  175

Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Leu Gly Ala Xaa Xaa Xaa Xaa Xaa  
                                   180                                  185                                  190

Gly Thr Arg  
                   195

<210> 46  
 <211> 60  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: A FabK Consensus Sequence

<220>  
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 <222> (2)..(2)  
 <223> X=Ile or Val

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(4)  
 <223> X=any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(5)  
 <223> X=Gly or Ala

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> X=Gly or Pro

<220>



Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val  
 50 55 60

<210> 47  
 <211> 1167  
 <212> DNA  
 <213> Staphylococcus aureus NCTC 8325

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 actcaaatgt taagtattga atatccaatt attacagcag gtttggcagg aagtacgacc 180  
 cccaaattag ttgcattaat taataacagt ggtggggttag gcacaatagg cgaggttac 240  
 tttaatacgc agcaattgga agatgaaata gattatgtac gccaatbaac gtcaaattct 300  
 tttggcgtaa atgtctttgt accaagtcaa caatcatata ccagtagtca aattgaaaat 360  
 atgaatgcat gggtaaaacc ttatcgacgc gcattacatt tagaagagcc ggttgtaaaa 420  
 attacccaag aacaacaatt taagtgtcat attgatacga taattaaaaa gcaagtgcct 480  
 gtatgttggt ttacttttgg aattccaagc gaacagatta taagcagggt gaaagcagcg 540  
 aatgtcaaac ttataggtac agcaacaagt gttgatgaag ctattgcgaa tgaaaaagcg 600  
 ggtatggatg ctatcgttgc tcaaggtagt gaagcagggtg gacatcgtgg ttcatTTTTA 660  
 aaacctaata atcaattacc tatggttggga acaatatctt tagtgccaca aattgtagat 720  
 gtcgtttcaa ttccgggtcat tgccgctggt ggaattatgg atggtagagg agttttggca 780  
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 agtaatgcat cagaactact gcgagatgca attataaata gtaaagaaac agatacagtc 900  
 attacaaaag cgtttagtgg aaagcttgca cgcggtatca acaatagggt tatcgaagaa 960  
 atgtcccaat acgaaggcga tatcccagat tatccaatac aaaatgagct aacaagtagc 1020  
 ataagaaaag ccgcagcaaa catcggcgac aaagagttaa tacatatgtg gagtggacaa 1080  
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 attaatacaa tcatgcaata taaataa 1167

<210> 48  
 <211> 355  
 <212> PRT  
 <213> Staphylococcus aureus NCTC 8325

<400> 48

Met Trp Asn Lys Asn Arg Leu Thr Gln Met Leu Ser Ile Glu Tyr Pro  
 1 5 10 15

Ile Ile Thr Ala Gly Leu Ala Gly Ser Thr Thr Pro Lys Leu Val Ala  
 20 25 30

Leu Ile Asn Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe  
 35 40 45

Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr  
 50 55 60

Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr  
 65 70 75 80

Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg  
 85 90 95

Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln  
 100 105 110

Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val  
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu  
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu  
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly  
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln  
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val  
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly  
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr  
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp  
 245 250 255



Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe  
 260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met  
 275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu  
 290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu  
 305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro  
 325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met  
 340 345 350

Gln Tyr Lys  
 355

<210> 49

<211> 753

<212> DNA

<213> FabI Bacillus subtilis

<400> 49

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gcagcattag aaacagcggg agaaatcgaa aagcttggcg ttaaagtgtc tgtcgtaaaa      180
gcaaacgtag gacagcctgc aaaaatcaaa gaaatgtttc agcaaattga tgaaacgttc      240
ggcagacttg atgtttttgt caataatgcc gcttcaggag tactaagacc tgtcatggaa      300
ttagaagaaa cacactggga ctggacgatg aacattaatg cgaaagcatt gcttttctgc      360
gctcaggaag ctgccaaagt aatggagaag aacggtggcg ggcataattgt cagcattagt      420
tcattaggct ctatccgcta tcttgaaaac tacaccacgg tcggtgtatc aaaagcagcg      480
ttagaggctt taaccggtta tcttgccgtt gagctttcac caaaacaaat tatcgtcaat      540
gctgtttcag gcggagcgat cgacacagat gcgctgaagc acttcccgaa tagagaagat      600
ctgcttgagg atgcgcgcca aaatacgccg gcgggacgca tggctcgaaat taaagacatg      660
gttgatactg tggagtttct agtgtcttcc aaggctgaca tgatccgcgg acagacaatt      720
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<210> 50  
 <211> 250  
 <212> PRT  
 <213> FabI Bacillus subtilis

<400> 50

Met Glu Gln Asn Lys Cys Ala Leu Val Thr Gly Ser Ser Arg Gly Val  
 1 5 10 15

Gly Lys Ala Ala Ala Ile Arg Leu Ala Glu Asn Gly Tyr Asn Ile Val  
 20 25 30

Ile Asn Tyr Ala Arg Ser Lys Lys Ala Ala Leu Glu Thr Ala Glu Glu  
 35 40 45

Ile Glu Lys Leu Gly Val Lys Val Leu Val Val Lys Ala Asn Val Gly  
 50 55 60

Gln Pro Ala Lys Ile Lys Glu Met Phe Gln Gln Ile Asp Glu Thr Phe  
 65 70 75 80

Gly Arg Leu Asp Val Phe Val Asn Asn Ala Ala Ser Gly Val Leu Arg  
 85 90 95

Pro Val Met Glu Leu Glu Glu Thr His Trp Asp Trp Thr Met Asn Ile  
 100 105 110

Asn Ala Lys Ala Leu Leu Phe Cys Ala Gln Glu Ala Ala Lys Leu Met  
 115 120 125

Glu Lys Asn Gly Gly Gly His Ile Val Ser Ile Ser Ser Leu Gly Ser  
 130 135 140

Ile Arg Tyr Leu Glu Asn Tyr Thr Thr Val Gly Val Ser Lys Ala Ala  
 145 150 155 160

Leu Glu Ala Leu Thr Arg Tyr Leu Ala Val Glu Leu Ser Pro Lys Gln  
 165 170 175

Ile Ile Val Asn Ala Val Ser Gly Gly Ala Ile Asp Thr Asp Ala Leu  
 180 185 190

Lys His Phe Pro Asn Arg Glu Asp Leu Leu Glu Asp Ala Arg Gln Asn  
 195 200 205

Thr Pro Ala Gly Arg Met Val Glu Ile Lys Asp Met Val Asp Thr Val  
 210 215 220

Glu Phe Leu Val Ser Ser Lys Ala Asp Met Ile Arg Gly Gln Thr Ile  
 225 230 235 240

Ile Val Asp Gly Gly Arg Ser Leu Leu Val  
 245 250

<210> 51  
 <211> 780  
 <212> DNA  
 <213> Campylobacter jejuni NCTC 11168 FabI

<400> 51  
 atgaatacag aatttcaagg aaaaacttta gtgattagcg gtggaactcg cgggataggc 60  
 aaagctatag tttatgaatt tgctaaagtg ggtgcaaata tagcttttac ttataattct 120  
 aatgcgcaaa ttgctgatga aatgggttcaa gatttggaga aaaattataa aatcaaagct 180  
 agagcttatg aatttaatat cttagaacct gaaacctata aagaactttt tgaaaaaatt 240  
 gatgtggatt ttgatagagt ggattatttt atctcaaagt ctatcatttc aggacgtgcg 300  
 gttgtaggtg gctataccaa atttatgaag ttaaaaccaa agggaattaa taacattttt 360  
 acagccacag taaatgcttt tgttgtgggc gcacaagaag cagctaaaag gatggaaaaa 420  
 gtaggggggtg gaagcattat ttctatctca tctacaggaa atttagtgta tatagaaaat 480  
 tattcaggtc acggtacagc aaaagccgct gtagaagcta tggcaagata tgcggctact 540  
 gaacttggag aaaaaaatat ccgtgtaaat gtcgtaagtg gtgggcctat taaaactgat 600  
 gctttaagag cttttacaaa ttatgaagaa gtaaaacagg ctactataaa ttttaagccct 660  
 ttaaactgca tggggcagcc tgaagatttg gctggagcat gtctttttct ttgttcaagt 720  
 aaggcaagtt ggggttacagg acatactttc atcgttgatg gtggtacaac ttttaaataa 780

<210> 52  
 <211> 259  
 <212> PRT  
 <213> Campylobacter jejuni FabI

<400> 52

Met Asn Thr Glu Phe Gln Gly Lys Thr Leu Val Ile Ser Gly Gly Thr  
 1 5 10 15

Arg Gly Ile Gly Lys Ala Ile Val Tyr Glu Phe Ala Lys Val Gly Ala  
 20 25 30

Asn Ile Ala Phe Thr Tyr Asn Ser Asn Ala Gln Ile Ala Asp Glu Met  
 35 40 45

Val Gln Asp Leu Glu Lys Asn Tyr Lys Ile Lys Ala Arg Ala Tyr Glu  
 50 55 60  
 Phe Asn Ile Leu Glu Pro Glu Thr Tyr Lys Glu Leu Phe Glu Lys Ile  
 65 70 75 80  
 Asp Val Asp Phe Asp Arg Val Asp Tyr Phe Ile Ser Asn Ala Ile Ile  
 85 90 95  
 Ser Gly Arg Ala Val Val Gly Gly Tyr Thr Lys Phe Met Lys Leu Lys  
 100 105 110  
 Pro Lys Gly Ile Asn Asn Ile Phe Thr Ala Thr Val Asn Ala Phe Val  
 115 120 125  
 Val Gly Ala Gln Glu Ala Ala Lys Arg Met Glu Lys Val Gly Gly Gly  
 130 135 140  
 Ser Ile Ile Ser Ile Ser Ser Thr Gly Asn Leu Val Tyr Ile Glu Asn  
 145 150 155 160  
 Tyr Ser Gly His Gly Thr Ala Lys Ala Ala Val Glu Ala Met Ala Arg  
 165 170 175  
 Tyr Ala Ala Thr Glu Leu Gly Glu Lys Asn Ile Arg Val Asn Val Val  
 180 185 190  
 Ser Gly Gly Pro Ile Lys Thr Asp Ala Leu Arg Ala Phe Thr Asn Tyr  
 195 200 205  
 Glu Glu Val Lys Gln Ala Thr Ile Asn Leu Ser Pro Leu Asn Arg Met  
 210 215 220  
 Gly Gln Pro Glu Asp Leu Ala Gly Ala Cys Leu Phe Leu Cys Ser Ser  
 225 230 235 240  
 Lys Ala Ser Trp Val Thr Gly His Thr Phe Ile Val Asp Gly Gly Thr  
 245 250 255  
 Thr Phe Lys

<210> 53  
 <211> 789  
 <212> DNA  
 <213> Helicobacter pylori FabI

<400> 53  
 atgaatgggtt ccaatcacat gaaaaataaa accctagtga tcagcggcgc gactagaggg 60  
 attggcaagg cgatatttgt acgcttcgct caaagcggcg tgaatatcgc ttctacttac 120  
 aataaaaaatg ttgaagaagc caacaaaatc atagaagatg tggagcaaaa atattccatt 180  
 aaagccaaag cctactctct taatgtttta gagcctgagc aatacacgga gcttttcaag 240  
 caaattgacg ctgattttga cagagtggat ttttttattt ctaacgctat tatttatggg 300  
 cgttctgtcg tgggggggatt tgcaccgttt atgcgattaa aacctaaggg gttaaacaac 360  
 atttacacag ccaccgtggt agcgttcgct gtaggggctc aagaagcggc aaaacgcatg 420  
 caaaaaatag gcggtggggc gatcgtgagc ttaagttcta ccgggaatct agtttatatg 480  
 cctaattacg ccgggcatgg caattccaaa aacgccgtag aaaccatggt caaatagcgt 540  
 gccgtggatt taggcgaatt taacattaga gtgaatgcgg ttagtggcgg gcctattgat 600  
 acggacgctt tgaaagcctt ccctgattat gtggagatta aagaaaaagt agaagagcaa 660  
 tcgcccctaa aacgcatggg caatcctaac gatctagccg gagcggctta ttttttatgc 720  
 gatgagaccc aaagcgggtg gcttacaggg caaacgatcg ttgtagatgg cgggactact 780  
 tttaaataa 789

<210> 54  
 <211> 262  
 <212> PRT  
 <213> *Helicobacter pylori* Fabl

<400> 54

Met Asn Gly Ser Asn His Met Lys Asn Lys Thr Leu Val Ile Ser Gly  
 1 5 10 15

Ala Thr Arg Gly Ile Gly Lys Ala Ile Phe Val Arg Phe Ala Gln Ser  
 20 25 30

Gly Val Asn Ile Ala Phe Thr Tyr Asn Lys Asn Val Glu Glu Ala Asn  
 35 40 45

Lys Ile Ile Glu Asp Val Glu Gln Lys Tyr Ser Ile Lys Ala Lys Ala  
 50 55 60

Tyr Ser Leu Asn Val Leu Glu Pro Glu Gln Tyr Thr Glu Leu Phe Lys  
 65 70 75 80

Gln Ile Asp Ala Asp Phe Asp Arg Val Asp Phe Phe Ile Ser Asn Ala  
 85 90 95

Ile Ile Tyr Gly Arg Ser Val Val Gly Gly Phe Ala Pro Phe Met Arg  
 100 105 110

Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val Leu Ala  
 115 120 125

Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys Ile Gly  
 130 135 140

Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val Tyr Met  
 145 150 155 160

Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu Thr Met  
 165 170 175

Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg Val Asn  
 180 185 190

Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala Phe Pro  
 195 200 205

Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro Leu Lys  
 210 215 220

Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe Leu Cys  
 225 230 235 240

Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val Val Asp  
 245 250 255

Gly Gly Thr Thr Phe Lys  
 260

<210> 55

<211> 843

<212> DNA

<213> FabI Streptomyces collinus

<400> 55

atgaacagcc ctcaccagca gcagaccgcc gaccgccggc aggtctccet gatcaccggg 60

gcctcgcgcg gcatcgggcg caccctggcc ctcaccctcg cccgccgggg tggcaccgtg 120

gtcgtcaact acaagaagaa cgccgacctg gcacagaaga ccgtcgccga ggctcaggag 180

gccggtggcc agggcttcgc ggtccaggcg gacgtcgaga ccaccgaggg ggctcaggcg 240

ctgttcgacg aggtggcgca gcgctcgggg aggctcgatc acttcgtctc caacgcggcg 300

gcgagcgcgt tcaagaacat cgtcgatctc ggcccgacc acctggaccg ctogtacgcg 360  
 atgaacctgc ggcccttcgt gctgggggcg caacaggccg tgaagctgat ggacaacggc 420  
 ggacggatcg tcgcgtgtc ctctacggc tcgggtccgc cctacccac ctacgcgatg 480  
 ctcggcggca tgaaagccgc catcgagtca tgggtgcggt acatggcggg ggagttcgct 540  
 ccttacggca tcaacgtcaa cgcgggtcaac ggcgccctga tcgactccga ttcgctggag 600  
 ttcttctaca acgtcgagg catgcgcgcc atgcaggcg tcctcgaccg catccccgcg 660  
 cgccgtccgg gcaccgtaca ggagatggc gacaccatcg ccttcctgct cggcgacgga 720  
 gcgggttaca tcaccgggca gaccctcgtg gtcgacggcg ggctcagcat cgtcgcgccg 780  
 ccgttcttcg cggacgcggg tgaggcgctc gagctgccg cccggccgac gcgagacgcc 840  
 tga 843

<210> 56  
 <211> 280  
 <212> PRT  
 <213> FabI Streptomyces collinus

<400> 56

Met Asn Ser Pro His Gln Gln Gln Thr Ala Asp Arg Arg Gln Val Ser  
1 5 10 15

Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Arg Thr Leu Ala Leu Thr  
20 25 30

Leu Ala Arg Arg Gly Gly Thr Val Val Val Asn Tyr Lys Lys Asn Ala  
35 40 45

Asp Leu Ala Gln Lys Thr Val Ala Glu Val Glu Glu Ala Gly Gly Gln  
50 55 60

Gly Phe Ala Val Gln Ala Asp Val Glu Thr Thr Glu Gly Val Thr Ala  
65 70 75 80

Leu Phe Asp Glu Val Ala Gln Arg Cys Gly Arg Leu Asp His Phe Val  
85 90 95

Ser Asn Ala Ala Ala Ser Ala Phe Lys Asn Ile Val Asp Leu Gly Pro  
100 105 110

His His Leu Asp Arg Ser Tyr Ala Met Asn Leu Arg Pro Phe Val Leu  
115 120 125

Gly Ala Gln Gln Ala Val Lys Leu Met Asp Asn Gly Gly Arg Ile Val

130		135		140
Ala Leu Ser Ser Tyr Gly Ser Val Arg Ala Tyr Pro Thr Tyr Ala Met				
145		150		155 160
Leu Gly Gly Met Lys Ala Ala Ile Glu Ser Trp Val Arg Tyr Met Ala				
	165		170	175
Val Glu Phe Ala Pro Tyr Gly Ile Asn Val Asn Ala Val Asn Gly Gly				
	180		185	190
Leu Ile Asp Ser Asp Ser Leu Glu Phe Phe Tyr Asn Val Glu Gly Met				
	195		200	205
Pro Pro Met Gln Gly Val Leu Asp Arg Ile Pro Ala Arg Arg Pro Gly				
	210		215	220
Thr Val Gln Glu Met Ala Asp Thr Ile Ala Phe Leu Leu Gly Asp Gly				
	225		230	235 240
Ala Gly Tyr Ile Thr Gly Gln Thr Leu Val Val Asp Gly Gly Leu Ser				
	245		250	255
Ile Val Ala Pro Pro Phe Phe Ala Asp Ala Gly Glu Ala Leu Glu Leu				
	260		265	270
Pro Pro Arg Pro Thr Arg Asp Ala				
	275		280	

<210> 57  
 <211> 176  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: A FabI Consensus Sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> X=Ala, Gly, Ser, Pro, or Thr

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> X=Pro, Ala, Gly, Thr, or Ser

<220>  
 <221> MISC\_FEATURE



<222> (6)..(6)  
<223> X=Ile, Val, Leu, or Met

<220>  
<221> MISC\_FEATURE  
<222> (8)..(127)  
<223> X=any amino acid and up to 20 may be absent

<220>  
<221> MISC\_FEATURE  
<222> (130)..(130)  
<223> X=Glu, Gln, Asn, or Asp

<220>  
<221> MISC\_FEATURE  
<222> (132)..(132)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (134)..(134)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (136)..(159)  
<223> X=any amino acid and up to 6 may be absent

<220>  
<221> MISC\_FEATURE  
<222> (161)..(166)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (168)..(168)  
<223> X=any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (170)..(170)  
<223> X=Val, Ile, Leu, or Met

<220>  
<221> MISC\_FEATURE  
<222> (172)..(172)  
<223> X=Thr, Ala, Ser, Pro, or Gly

<220>  
<221> MISC\_FEATURE  
<222> (173)..(174)

<223> X=any amino acid

<220>

<221> MISC\_FEATURE

<222> (175)..(175)

<223> X=Lys, Arg, or His

<400> 57

Gly Xaa Xaa Arg Gly Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala  
115 120 125

Gln Xaa Ala Xaa Lys Xaa Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Tyr  
165 170 175

<210> 58

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabI Consensus Sequence

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> X=Ala, Gly, Ser, Pro, or Thr

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> X=Pro, Ala, Gly, Thr, or Ser

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> X=Ile, Val, Leu, or Met

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> X=any amino acid

<400> 58

Gly Xaa Xaa Arg Gly Xaa Gly Xaa  
1 5

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 59

tctagacata tgaaaacgcg tattacagaa tta

33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 60

ggatcctaga tactgggcac cttgacc

27

<210> 61

<211> 5

<212> PRT

<213> Unknown

<220>  
<223> Description of Unknown Organism: A SDR Consensus Sequence

<220>  
<221> MISC\_FEATURE  
<222> (2)..(4)  
<223> X=any amino acid

<400> 61

Tyr Xaa Xaa Xaa Lys  
1 5

<210> 62  
<211> 8  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: A Enoyl Reductase Consensus Sequence

<220>  
<221> MISC\_FEATURE  
<222> (2)..(7)  
<223> X=any amino acid

<400> 62

Thr Xaa Xaa Xaa Xaa Xaa Lys  
1 5